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Régujt
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq length: 0
seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Published_Applications_AA_New:*
1: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
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Gapop 10.0 , Gapext 0.5
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                                         KKRYDREFLLGF 12
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Copyright (c) 1993 - 2005 Compugen Ltd.
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          169
478
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718
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10027
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                                     US-10-131-826A-412
US-10-793-626-76
US-10-821-234-1234
US-10-821-234-915
US-11-821-174-176-98
US-11-0793-626-3184
US-10-793-626-3184
US-10-793-626-3236
US-11-074-176-306
US-11-074-176-306
US-11-074-176-312
US-10-793-626-3324
US-10-793-626-3324
US-10-793-626-211
US-10-793-626-211
US-10-793-626-2418
US-10-793-626-2418
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US-10-793-626-2418
US-10-793-626-1990
US-11-090-878-10
US-11-090-878-10
US-10-793-626-1212
US-10-793-626-1212
US-10-793-626-1212
US-10-793-626-1212
         US-10-793-626-1212
US-10-793-626-190
US-10-821-234-1393
US-10-981-873-44
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12.124 Million cell updates/sec
                       Sequence 412, App
Sequence 746, Appl
Sequence 715, App
Sequence 915, App
Sequence 915, App
Sequence 3112, App
Sequence 3114, App
Sequence 3184, App
Sequence 3236, App
Sequence 326, App
Sequence 3216, App
Sequence 324, App
Sequence 3324, App
Sequence 211, Appl
Sequence 211, Appl
Sequence 211, App
Sequence 211, App
Sequence 190, App
Sequence 190, App
Sequence 190, App
Sequence 191, Appl
Sequence 191, App
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1393, ...
Appl
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APPLICANT:

APPLICANT:

APPLICANT:

Stewart, Timothy A. Tumas, Daniel Smith, Victoria Sherwood, Steven Godowski, Paul J. Gurney, Austin L. Goddard, Audrey Gerritsen, Mary E. Gao, Wei-Qiang Desnoyers, Luc Filvaroff, Ellen

APPLICANT: APPLICANT: APPLICANT:

APPLICANT: APPLICANT:

APPLICANT:

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26
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Sequence 10, Appl	Sequence 2, Appli	Sequence 4, Appli	Sequence 20, Appl		Sequence 14, Appl	Sequence 914, App	•	Sequence 234, App	,	≥		Sequence 334, App	Þ	-	Sequence 11, Appi	٠,٠	•	•	Sequence 1443, Ap

## ALIGNMENTS

GENERAL INFORMATION: Publication No.

Application US/10131826A US20050245730A1

APPLICANT: Baker, Kevin P. APPLICANT: Beresini, Maur

Beresini,Maureen

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APPLICANT: ENGL, CALLER APPLICANT: STANGE, CONTROL SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C128
CURRENT FAPLICATION NUMBER: 60/0410/131,826A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR APPLICATION NUMBER: 60/059117
PRIOR APPLICATION NUMBER: 60/059117
PRIOR APPLICATION NUMBER: 60/059117
PRIOR APPLICATION NUMBER: 60/059122
PRIOR APPLICATION NUMBER: 60/059122
PRIOR APPLICATION NUMBER: 60/059184
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-19
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR APPLICATION NUMBER: 60/059588
PRIOR APPLICATION NUMBER: 60/059588
PRIOR APPLICATION NUMBER: 60/059588
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Prior Application data removed - See File Wrapper or PALM.
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Wood, William
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FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PACENTIN Ver. 2.1
SEQ ID NO 746
LENGTH: 297
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: TENEORMATTION: Description of Artificial
                                                                                                                                                                                                                                                                                                                                                                                                     US-10-793-626-746
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OTHER INFORMATION: Description of Artificial Sequence: synthetic

OTHER INFORMATION: amino acid sequence

US-10-793-626-66
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US-10-793-626-66
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US-10-131-826A-412
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TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERWIDIS NUCLEIC ACIDS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CÜRRENT FILING DATE: 2004-03-04
PAIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PAtentin Ver. 2:1
SEQ ID NO 66
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Best Local Similarity
""" hes 7; Conserv
                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 66, Application US/10793626
Publication No. US2005025478A1
GENERAL INFORMATION:
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SEQ ID NO 412
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                   OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: amino acid sequence
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TYPE: PRT
ORGANISM: Artificial Sequence
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70.0%;
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Pred. No. 22;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
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Pred. No. 14;
 Score 33;
Pred. No.
 DB
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                Length 297;
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FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt SEQ_genes Version 1.0
SEQ ID NO 1234
LENGTH: 169
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; NAME/KEY: misc feature
; LOCATION: (1)...(169)
; OTHER INFORMATION: Xaa = any amino acid or nothing
US-10-821-234-1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                         ; ORGANISM: Homo sapiens US-10-821-234-915
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                                                                                                                                        SOFTWARE: pt_SEQ_genes Version 1.0
SEQ ID NO 915
LENGTH: 478
TYPE: PRT
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Publication No. US20050255114A1
GENERAL INFORMATION:
                                   Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 915, Application US/10821234
Publication No. US20050255114A1
                                                                    Query Match
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APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
                                                                                                                                                                                                                                                                                            APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 1704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 85.
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     1 KKRYDREFL 9
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                                      Conservative
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••
                                                      Score 32;
Pred. No.
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Pred. No. 12;
                                          Mismatches
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                                                                        Length 478;
                                        Indels
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384 REAYDRDFL 392

RESULT 6 US-11-074-176-98

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APPLICANT: Russell, William M.
APPLICANT: Russell, William M.
APPLICANT: Altermann, Eric
APPLICANT: Altermann, Eric
APPLICANT: McAuliffe, Olivia
APPLICANT: Peril, Andrea Azcarate
TITLE OF INVENTION: Nucleic Acid Sequences Encoding
TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
FILE REPERENCE: 5051-694
CURRENT APPLICATION NUMBER: US/11/074,176
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: 60/551,161
PRIOR APPLICATION NUMBER: 60/551,161
PRIOR APPLICATION NUMBER: 5051-161
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 98
ILBNG DATE: 2004-03-08
SEQ ID NO 98
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US-11-074-176-98
                                                           US-10-793-626-3184
                                                                              RESULT 8
                                                                                                                                                                                                                                                                                                       US-10-793-626-3112
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                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 3112
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Sequence 3184, Application US/10793626 Publication No. US20050255478A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                          Query Match
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TITLE OF INVENTION: STARHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PUJ480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
                                                                                                                                                                                                                                                                                                       FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: amino acid sequence
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TYPE: PRT
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                                                                                                                                        118 KRHKQTFLLG 127
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Similarity 60.0%;
6; Conservative
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; Pred. No. 33;
2; Mismatches
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US-10-793-626-3236
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Best Local S
Matches 5
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PRIOR FILING DATE: 2004-07-27
NUMBER OF SEQ ID NOS: 117
SOFTWARE: FASTSEQ FOR Windows Version 4.0
SEQ ID NO 41
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Sequence 3236, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
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TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Walensky, Loren D.
APPLICANT: Korsmeyer, Stanley J.
APPLICANT: Verdine, Gregory
TITLE OF INVENTION: STABILIZED ALPHA HELICAL PEPTIDES AND
TITLE OF INVENTION: USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 00530-124001
CURRENT APPLICATION NUMBER: US/10/981,873
CURRENT FILING DATE: 2004-11-05
PRIOR APPLICATION NUMBER: US 60/517,848
PRIOR FILING DATE: 2003-11-05
PRIOR FILING DATE: 2003-11-05
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ORGANISM: Artificial Sequence
FEATURE:
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RESULT 11
US-11-074-176-306
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TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
FILE REFERENCE: 5031-694
CURRENT APPLICATION NUMBER: US/11/074,176
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: 60/551,161
PRIOR FILING DATE: 2004-03-08
NUMBER OF SEQ ID NOS: 381
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 306
LENGTH: 718
                                                                                                                                                                                                                                                                             Sequence 18, Application US/11074176
Publication No. US20050250135A1
GENERAL INFORMATION:
APPLICANT: Klaenhammer, Todd R.
APPLICANT: Russell, William M.
APPLICANT: Altermann, Eric
APPLICANT: McAuliffe, Olivia
APPLICANT: McAuliffe, Mc
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3236
LENGTH: 411
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Best Local (
FILE REFERENCE: 5051-694
CURRENT APPLICATION NUMBER: US/11/074,176
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: 60/551,161
PRIOR FILING DATE: 2004-03-08
NUMBER OF SEQ ID NOS: 381
SOPTWARE: FASTSEQ for Windows Version 4.0
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Local Similarity 75.0%;
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Pred. No. 64;
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Pred. No. 1.1e+02;
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                  Query Match
Best Local Similarity
Thes 6; Conserve
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Best Local Similarity
Watches 6; Conserve
                                                                                                      ORGANISM: Rabbit sp. US-11-057-058-62
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                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-793-626-3324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAFHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION UNMBER: 60/164,258
PRIOR APPLICATION UNMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 3324
LENGTH: 944
TYDE: DET
                                                                                                                                                                                                                                                                                                                                                                    Sequence 62, Application US/11057058 Publication No. US20050244400A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3324, Application US/10793626 Publication No. US20050255478A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 5; Conserv
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LENGTH: 723
                                                                                                                                                                        SOFTWARE: PatentIn version 3.3 SEQ ID NO 62
                                                                                                                                                                                                                                                APPLICANT: Maga, John
TITLE OF INVENTION: ACID ALPHA-GLUCOSIDASE AND FRAGMENTS THEREOF
FILE REFERENCE: SYM-011
CURRENT APPLICATION NUMBER: US/11/057,058
CURRENT FILING DATE: 2005-02-10
CURRENT FILING DATE: 2005-02-10
                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/543,812
PRIOR FILING DATE: 2004-02-10
NUMBER OF SEQ ID NOS: 68
                                                                                                                                                                                                                                                                                                                                     APPLICANT: LeBowitz, Jonathan APPLICANT: Maga, John
                                                                                                                                           LENGTH: 1
TYPE: PRT
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   767 KRYNRETL 774
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 5 DREFLLG 11
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                                                   Score 30; DB 7;
Pred. No. 2.6e+02;
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Pred. No. 1.4e+02;
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Pred. No. 1.1e+02
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                                                                   Length 1827;
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RESULT 15

US-10-821-234-916

US-10-821-234-916

Sequence 916, Application US/10821234

Publication No. US20050255114A1

GENERAL INFORMATION:

APPLICANT: Labat, Ivan
APPLICANT: Eabat, Ivan
APPLICANT: Eabat, Ivan
APPLICANT: Eabat, Ivan
APPLICANT: Eabat, Ivan
APPLICANT: Tang, Y. Tom
ITILE OF INVENTION: Methods for Disgnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2003-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR APPLICATION NUMBER: US 60/462,047

PRIOR APPLICATION NUMBER: US 704

SOFTWARE: PET 2003-04-07

RUMBER OF SEQ ID NOS: 1704
SOFTWARE: PET 2003-04-07

CORANIEM: Homo sapiens
US-10-821-234-916

Ouery Match

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3 RYDREFLIG 11
Db 2979 KYDKOVLSG 2987

Search completed: November 29, 2005, 23:04:37

Job time: 3.25 secs
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Maximum Match 100%
Listing first 45 summaries
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seq length: 2000000000
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Match
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Gapop 10.0 , Gapext 0.5
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64
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Published Applications AA Main.*

| (Ggn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
| (Ggn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
| (Ggn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
| (Ggn2_6/ptodata/1/pubpaa/USIOA_PUBCOMB.pep:*
| (Ggn2_6/ptodata/1/pubpaa/USIOA_PUBCOMB.pep:*
| (Ggn2_6/ptodata/1/pubpaa/USI1_PUBCOMB.pep:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-973-473-9.
US-09-973-473-11
US-09-973-473-10
US-09-973-473-10
US-10-450-763-5079
US-10-335-977-6270
US-10-335-977-6271
US-10-427-973-11493
US-10-425-115-282367
US-10-425-115-282367
US-10-425-115-282367
US-10-425-115-288687
US-10-425-115-2816887
US-10-425-115-282-4466
US-10-501-282-4466
US-10-501-282-4466
US-10-501-282-4466
US-10-425-115-357901
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Sequence 11, Appl
Sequence 10, Appl
Sequence 50799, A
Sequence 9703, Ap
Sequence 6269, Ap
Sequence 6270, Ap
Sequence 6271, Ap
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Sequence
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a 312, App

a 187843,

a 69, Appl

a 116, Appl

a 12, Appl

b 12, Appl

b 288687,

a 1519449,

a 151949,

b 4464, Ap

b 4464, Ap

a 4464, Ap

a 42944, A

a 42944, A

a 55721, A

a 55721, A

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37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37
57.8	57.8	57.8	57.8	57.8	57.8	57.8	57.8	57.8	57.8	57.8	57.8	57.8	57.8	57.8	57.8	57.8	57.8
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US-09-833-245-1304	US-10-282-122A-65941	US-10-425-114-43422	US-10-767-701-36815	US-10-138-898-106	US-10-405-660-106	US-10-400-902-24	US-10-139-218-106	US-10-139-296-106	US-10-138-916-106	US-10-138-905-106	US-10-139-031-106	US-10-138-838-106	US-09-976-800-106	US-09-911-781-24	US-10-425-115-328208	US-10-437-963-154057	US-10-767-701-51018
Sequence 1304, Ap		Sequence 43422, A		Sequence 106, App	Sequence 106, App	➣	_	•	Sequence 106, App	•	Sequence 106, App		Sequence 106, App		B.1	Sequence 154057,	Sequence 51018, A

ALIGNMENTS

### APPLICANT: SONEMBERG, Nahum APPLICANT: TREMBLAY, MICHAI APPLICANT: TREMBLAY, MICHAI APPLICANT: TSUKIAYAMA-KOHARA, KYOKO TITLE OF INVENTION: NON-HUMAN TRANSGENIC ANIMP TITLE OF INVENTION: ENCODING 4E-BP1 FILE REFERENCE: 51401200400 CURRENT APPLICATION NUMBER: US/09/973,473 CURRENT APPLICATION NUMBER: US/09/973,473 CURRENT FILING DATE: 2001-10-03 PRIOR APPLICATION NUMBER: 6C7/CA00/00388 PRIOR APPLICATION NUMBER: 60/128,559 PRIOR APPLICATION NUMBER: 60/128,559 PRIOR APPLICATION NUMBER: 60/179,743 US-09-973-473-11 Sequence 11, Application US/09973473 Sequence 11, Application US/09973473 Publication No. US20030041341A1 GENERAL INFORMATION: APPLICANT: SONENBERY, Mahum APPLICANT: TREMBLAY, Michel APPLICANT: TSUKIAYAMA-KOHARA, KYOKO TITLE OF INVENTION: NON-HUMAN TRANSGENIC ANIMAL WHOSE GERM CELLS AND TITLE OF INVENTION: SONATIC CELLS CONTAIN A KNOCKOUT MUTATION IN DNA TITLE OF INVENTION: ENCODING 48-BP1 FILE REFERENCE: 514012000400 FILE REFERENCE: 514012000400 US-09-973-473-9 ; ORGANISM: Homo sapiens US-09-973-473-9 밁 RESULT 2 Query Match Best Local S Matches 12 Sequence 9, Application US/09973473 Publication No. US20030041341A1 GENERAL INFORMATION: LENGTH: 16 TYPE: PRT CURRENT APPLICATION NUMBER: US/09/973,473 12; 16 1 KKRYDREFLLGF 12 Similarity KKRYDREFLLGF 12 Conservative 100.0%; 0 Score 64; DB 3; Length 16; Pred. No. 9.7e-05; ); Mismatches 0; Indels ANIMAL WHOSE GERM CELLS AND MUTATION IN DNA 0; Gaps

0

CURRENT FILING DATE:

2001-10-03

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APPLICANT: SOMENBERG, Nahum
APPLICANT: TREMBLAY, Michel
APPLICANT: TREMBLAY, Michel
APPLICANT: TREMBLAY, Michel
APPLICANT: TSUKIAYAMA-KOHARA, KYOKO
TITLE OF INVENTION: NON-HUMAN TRANSGENIC ANIMAL WHOSE GERM CELLS AND
TITLE OF INVENTION: SOMATIC CELLS CONTAIN A KNOCKOUT MUTATION IN DNA
TITLE OF INVENTION: ENCODING 4E-BP1
FILE REFERENCE: 514012000400
FILER REFERENCE: 514012000400
CURRENT PILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: US/09/973,473
CURRENT PILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 60/128,559
PRIOR APPLICATION NUMBER: 60/128,559
PRIOR FILING DATE: 1999-04-09
PRIOR FILING DATE: 2000-02-02
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: PCT/CA00/00388
PRIOR FILING DATE: 2000-04-07
PRIOR PELLING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 60/128,559
PRIOR APPLICATION NUMBER: 60/179,743
PRIOR APPLICATION NUMBER: 60/179,743
PRIOR FILING DATE: 2000-02-02
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 16
TYPE: PRT
ORGANISM: Danio rerio
US-09-973-473-11
        RESULT 4
US-10-450-763-50799
US-10-450-763-50799, Application US/10450763
; Sequence 50799, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
    APPLICANT: Hyseq, Inc
    FILE REFERENCE: 790CIP3/US
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION UNMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR APPLICATION NUMBER: PCT/US01/08631
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-973-473-10
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US-09-973-473-10
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Publication No.
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PRIOR FILING DATE: 2001-03-30
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Pred. No. 0.01;
1; Mismatches
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Pred. No. 9.7e-05;
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PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILLING DATE: 2000-03-31
PRIOR PRIOL PRIOL NUMBER: 09/649,167
PRIOR FILLING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 50799
LENGTH: 1756
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; OTHER INFORMATION: Xaa = X or * as defined in Table US-10-450-763-50799
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US-10-335-977-9703
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Publication No. US20040052799A1

GENERAL INFORMATION:
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Best Local Similarity 83.3%;
Matches 10; Conservative
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NAME/KEY: DOMAIN
LOCATION: (49)..(59)
OTHER INFORMATION: TYPE I ANTIFREEZE PROTEIN SIGNATURE domain identified by
OTHER INFORMATION: eMATRIX, accession number PR00308C, p-value=8.013e-09, ra
OTHER INFORMATION: 3.83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: DOMAIN
LOCATION: (1689)..(1756)
OTHER INFORMATION: eIF4-gamma/eIF5/eIF2-epsilon domain identified by PFam,
OTHER INFORMATION: accession name IF5_eIF4_eIF2, E-value=0.0038, PFam scor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: (1)...(1756)
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                                     TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 9703:
                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: WINDOWS NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION NUMBER: 08/93,002
PRIOR APPLICATION NUMBER: 08/93,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             790 KKQYDREFLLDF 801
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                               TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 53; DB
Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...226
SEQUENCE DESCRIPTION: SEQ ID NO: 9703:
US-10-335-977-9703
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                                          US-10-335-977-6269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6269, Application US/10335977
Sequence 6269, Application US/10335977
Publication No. US20040052799A1

GENERAL INFORMATION:
GENERAL INFORMATION: NUCLEIC ACID AMINO ACID SEQUENCES
TITLE OF INVENTION: NUCLEIC ACID AM AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Query Match
                                                                                                                                                                                                                                                                                                         TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 6269:
                                                                                                                                                                                                                                                                                                                                                                   PILING DATE: 30-Dec-2002

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993,002

FILING DATE: 17-DEC-1997

ATTORNEY/AGENT INFORMATION:
NAME: Mandaragouras, Amy E.
REGISTRATION NUMBER: 35,207

REFERENCE/DOCKET NUMBER: GTN-018

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM IS09660
COMPUTER: IBM PC COMPARTIBLE
OPERATING SYSTEM: WINDOWS NT 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: UNIX
CURRENT APPLICATION NUMBER: US/10/335,977
APPLICATION NUMBER: US/10/335,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                           NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...339
SEQUENCE DESCRIPTION: SEQ ID NO: 620
                                                                                                                       FEATURE:
                                                                                                                                                                MOLECULE TYPE: protein HYPOTHETICAL: YES ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                          LENGTH: 339 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02109-1875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 226 amino acide
                                                                                                                                             ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68.8%;
    68.8%; Score 44; DB 4;
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Pred. No. 7
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                                                              6269:
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  Length 339;
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RESULT 8
US-10-335-977-6271
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; LOCATION: (B) LOCATION 1...553
; SEQUENCE DESCRIPTION: SEQ ID NO: 6270:
US-10-335-977-6270
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US-10-335-977-6270
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Publication No. US20040052799A1

GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 6270:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
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                                                                                                                                                         Matches
                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: WINDOWS NT 4.0
SOPTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION UNMBER: 08/993,002
APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          210 KKRYEKEFNLLWVGLLGF 227
                                                                              369 KKRYEKEFNILWVGLLGF 386
                                                                                                                                                         10;
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                                                                                                                 1 KKRYDREF-----LLGF 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                 ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55.6%; Pred. No. 11; ative 2; Mismatches
                                                                                                                                                                          55.6%;
                                                                                                                                                       2
                                                                                                                                                                            Score 44; DB
Pred. No. 18;
                                                                                                                                                             Mismatches
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                                                                                                                                                                                              Length 553;
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Sequence 6271, Application US/10335977 Publication No. US20040052799A1 GENERAL INFORMATION:

APPLICANT: DOUGLAS SMITH et al

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US-10-437-963-114937
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LOCATION: (B) LOCATION 1...556
SEQUENCE DESCRIPTION: SEQ ID NO: 6271:
US-10-335-977-6271
                                                                                                                                                                                                                                                                                             Sequence 114937, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
SEQ ID NO 114937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                    APPLICANT:
                                  TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
                                                                                                                                                                                                                                APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K. APPLICANT: Zhou, Yihua
                                                                                                                                                                           APPLICANT:
                    NUMBER OF SEQ ID NOS: 204966
                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 6271: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,20
REFERENCE/DOCKET NUMBER: C
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                      372 KKRYEKEFNLLWVGLLGF 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KKRYDREF-----LLGF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                       Cao, Yor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC Compatible OPERATING SYSTEM: Windows NT 4.0
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                                                                                                                                    Li, Ping
                                                                                                                                                  Boukharov, Andrey
Barbazuk, Brad
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                                                                                                                                                                                                             Yongwei
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55.6%;
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Pred. No. 18;
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US-10-425-115-282367
; Sequence 282367, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Thes 8; Conserve
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; OTHER INFORMATION: Clone US-10-437-963-114937
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US-10-259-194A-312
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                                                                                                                                                                                                        RESULT 11
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CURRENT APPLICATION NUMBER: US/10/259,194A
CURRENT FILING DATE: 2003-01-07
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/370,743
PRIOR FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: US 60/370,620
PRIOR APPLICATION NUMBER: US 60/370,620
PRIOR APPLICATION NUMBER: US 60/370,620
PRIOR FILING DATE: 2002-04-04
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SOFTWARE: PatentList.pl version 3.0.4 (C) 2001 Syngenta
SEQ ID NO 312
LENGTH: 941
TYPE: PRT
                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                               Query Match
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CURRENT APPLICATION NUMBER: US/10/425,115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ricke, Darrell
APPLICANT: Zhu, Tong
TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
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7; Conserv
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Briggs, Steven P.
Cooper, Bret
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Provart, Nicholas
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Pred. No. 1.7e+02,
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Pred. No.
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                                                    Other Molecules Associated With
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 282367
LENGTH: 950
TYPE: PRT
ORGANISM: Zea maye
FEATURE:
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                                                                                                                                                                   US-10-334-143-69

; Sequence 69, Application US/10334143
; Publication No. US20040009549A1
; GENERAL INFORMATION:
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Best Local Similarity
Marches 7; Conserve
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Best Local Similarity 72...
Conservative
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SEQ ID NO 187843
LENGTH: 1516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: GRIGORIEV, IGOR VYACHESLAVOVICH
APPLICANT: SUDARSANAM, SUCHA
TITLE OF INVENTION: METHOD FOR DETECTING REMOTE HOMOLOGUES:
TITLE OF INVENTION: KINASES IDENTIFIED WITH THE METHOD
FILE REFERENCE: 038602/1543
CURRENT APPLICATION NUMBER: US/10/334,143
CURRENT FILING DATE: 2002-12-31
PRIOR APPLICATION NUMBER: 60/343,169
PRIOR FILING DATE: 2001-12-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K. APPLICANT: Zhou, Yihua
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NAME/KEY: unsure
LOCATION: (1).. (1516)

OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                                                                                                                                                                                             552 RKRYSRDFLL 561
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Cao, Yongwei
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70.0%;
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Pred. No. 2.8e+02;
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APPLICANT: TREMBLAY, MICHEL
APPLICANT: TREMBLAY, MICHEL
APPLICANT: TSUKIAYANA-KOKARA, KYOKO
FITTLE OF INVENTION: NON-HUMAN TRANSCENIC ANIMAL WHOSE GERM CELLS AND
FITTLE OF INVENTION: SOMATIC CELLS CONTAIN A KNOCKOUT MUTATION IN DNA
FITTLE OF INVENTION: ENCODING 4E-BP1
FILLE OF INVENTION: ENCODING 4E-BP1
FILLE OF INVENTION NUMBER: US/09/973,473
CURRENT FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: PCT/CA00/00388
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 60/128,559
PRIOR APPLICATION NUMBER: 60/128,559
PRIOR APPLICATION NUMBER: 60/179,743
PRIOR APPLICATION NUMBER: 60/179,743
PRIOR FILING DATE: 2000-02-02
NUMBER OF SEQ ID NOS: 27
PRIOR FILING DATE: 2000-02-02
                                                                                                                                                                                                                                                                                                                                                 RESULT 15
US-09-973-473-12
; Sequence 12, Application US/09973473
; Publication No. US20030041341A1
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US-10-783-528-116
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Best Local Similarity
Matches 7; Conserv
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APPLICANT: SONENBERG, Nahum
APPLICANT: TREMBLAY, Michel
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Matches 7; Conservative
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APPLICANT: Gish, Kurt
APPLICANT: Wilson, Keith
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND
FILE REFERENCE: 05882.0191.NBUS01
CURRENT APPLICATION NUMBER: US/10/783,528
CURRENT FILING DATE: 2004-02-19
NUMBER OF SEQ ID NOS: 116
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TYPE: PRT
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TYPE: PRT
ORGANISM: Homo Sapiens
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FEATURE:
NAME/KEY: MOD RES
LOCATION: (2479)
OTHER INFORMATION: Variable amino acid
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2; Mismatches
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Pred. No. 4.7e+02;
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Maximum Match 100%
Listing first 45 summaries
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  pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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  protein search, using
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Match Length DB
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2: /cgn2 6/ptodata/1/iaa/6_COMB.pep:*

3: /cgn2 6/ptodata/1/iaa/H_COMB.pep:*

4: /cgn2 6/ptodata/1/iaa/PCTUS_COMB.pep:*

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                    5204252-4
US-09-270-767-55264
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US-09-2640-14261
US-08-954-333-7
US-08-954-796A-19839
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US-09-199-016-10766
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US-09-199-016-10766
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US-09-194-016-18814
US-09-248-796A-18814
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                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Appli
Sequence 85.8, Ap
Sequence 27703, A
Sequence 106, App
Sequence 24, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence 24, Appl
Patent No. 5204252
Patent No. 5204252
                                          Sequence 40048, A Sequence 14261, A Sequence 14261, A Sequence 19839, A Sequence 8459, Appli Sequence 8459, Appli Sequence 8, Appli Sequence 8, Appli Sequence 607, Appli Sequence 64, Appl Sequence 64, Appl Sequence 4393, Ap Sequence 1814, A Sequence 29351, A Sequence 29351, A Sequence 29351, Ap Sequence 29351, Ap Sequence 29351, Ap Sequence 29351, Ap Sequence 2739, Ap
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## ALIGNMENTS

RESULT 1 US-09-264-512B-2

Sequence 2, Application US/09264512B Patent No. 6610508

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Sequence 8518, Application US/09949016

Sequence 8518, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 00/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FBASTSEQ for Windows Version 4.0

SEQ ID NO 8518

LENGTH: 977
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US-09-949-016-8518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Hentze, Matthias W.
APPLICANT: Hentze, Matthias W.
APPLICANT: Hentze, Matthias W.
APPLICANT: Hentze, Matthias W.
APPLICANT: De Gregorio, Ennio
TITLE OF INVENTION: TRANSLATION DRIVER SYSTEM AND METHODS FOR USE THEREOF
FILE REPERENCE: 9882-004
CURRENT APPLICATION NUMBER: US/09/264,512B
CURRENT FILING DATE: 1999-03-08
UNDBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
LENGTH: 1560
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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Pred. No. 0.0015;
0; Mismatches 0;
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APPLICANT: Madduri, Krishna M.
APPLICANT: Cornett, Cathy A.
APPLICANT: Erenner, Alfred A.
APPLICANT: Tang, Maria
APPLICANT: Tang, Maria
APPLICANT: Loper, John C.
APPLICANT: Loper, John C.
APPLICANT: Loper, John C.
APPLICANT: Loper, John C.
TITLE OF INVENTION: CYTCCHROME P450 MONCOXYGENASE AND NADPH CYTCCHROME P450
TITLE OF INVENTION: HYDROXYLASE COMPLEX OF CANDIDA TROPICALIS AND METHODS
TITLE OF INVENTION: RELATING THERETO
FILE REFERENCE: 1010-16.seq
CURRENT APPLICATION NUMBER: US/09/302,620B
CURRENT APPLICATION NUMBER: US/09/302,620B
CURRENT APPLICATION NUMBER: 1999-04-30
NUMBER OF SEQ ID NOS: 109
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 199-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 27703
LENGTH: 82
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
US-09-302-620B-106
; Sequence 106, Application US/09302620B
; Patent No. 6331420
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: UNSURE
; LOCATION: (10)
GOTHER INFORMATION: Identity of amino acid sequences at the above locations are unknous-
US-09-248-796A-27703
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US-09-248-796A-27703
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US-09-949-016-8518
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Best Local Similarity
Matches 10; Conser
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                  APPLICANT: Wilson, C. Ron
APPLICANT: Craft, David L.
APPLICANT: Eirich, Dudley
APPLICANT: Eshoo, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Candida albicans FEATURE:
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Pred. No. 0.12;
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     175 DREFVIGE 182
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APPLICANT: Craft, David L.
APPLICANT: Wilson, C. Ron
APPLICANT: Eirich, Dudley
APPLICANT: Eirich, Dudley
APPLICANT: Zhang, Yeyan
TITLE OF INVENTION: USE OF CYP52A2A PROMOTER TO
FILE REFERENCE: U0012 OS/OAAP (1010-49)
CURRENT APPLICATION NUMBER: US/09/911,781
CURRENT FILING DATE: 2001-07-24
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.1
SEQ ID NO 24
LENGTH: 267
TYPE: PRT
                                                                                               SOPTWARE: PatentIn version 3.1
SEQ ID NO 24
LENGTH: 267
TYPE: PRT
ORGANISM: Candida tropicalis
US-10-400-902-24
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Best Local Similarity
Watches 6; Conserve
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                                                                                                                                                                                                             Sequence 24, Application US/10400902

Patent No. 6790640

GENERAL INFORMATION:
APPLICANT: Craft, David L.
APPLICANT: Wilson, C. Ron
APPLICANT: Eirich, Dudley
APPLICANT: Zhang, Yeyan
TITLE OF INVENTION: USE OF CYP52A2A PROMOTER TO INCREASE GENE EXPRESSION IN YEAST
FILE REFERENCE: U0012 OS/OAAP (1010-49)
CURRENT FILING DATE: 2003-03-31
PRIOR APPLICATION NUMBER: US/09/911,781
PRIOR PILING DATE: 2001-07-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 24, Application US/09911781
Patent No. 6673613
GENERAL INFORMATION:
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                             Local Similarity tes 6; Conserv
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RESULT 8
5204252-4
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;PATONIC CREGG, JAMES M.;GLEESON, MARTIN A.;HAAS, LISA
;PICATAGGIO, STEPHEN
TITLE OF INVENTION: CANDIDA TROPICALIS TRANSFORMATION SYSTEM
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PATENT NO. 5204252

PARTICANT: CREGG, JAMES M.; GLEESON, MARTIN A.; HAAS, LISA
PICATAGGIO, STEPHEN
TITLE OF INVENTION: CANDIDA TROPICALIS TRANSFORMATION SYSTEM
UMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/386,837
FILING DATE: 27-JUL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 308,481
; FILING DATE: 08-FEB-1989
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                                                                       Sequence 40048, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 625.7
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 40048
LENGTH: 347
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserv
-09-270-767-40048
                                           TYPE: PRT ORGANISM: Drosophila melanogaster
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APPLICATION NUMBER: 308,481
FILING DATE: 08-FEB-1989
             OTHER INFORMATION: Xaa
                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/07/386,837 FILING DATE: 27-JUL-1989
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nilarity 75.0%;
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Pred. No.
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Mysococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEO ID NO 14261
LENGTH: 347
TYPE: no.
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US-09-270-767-55264
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                                                                                                                  ; ORGANISM: Myxococcus xanthus
US-09-902-540-14261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 55264

LENGTH: 347

TYPE: PRT
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Best Local (
                                                       Best Local Similarity
Matches 7; Conserv
                                                                                     Query Match
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120 KSFDREFLL 128
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                             2 KRYDREFLL 10
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77.8%;
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                                                                        Score 37; pred. No.
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Pred. No. 46;
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RESULT 12 US-08-954-333-7

; Sequence 7, Application US/08954333

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FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 19839
LENGTH: 602
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknous-09-248-796A-19839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-248-796A-19839
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Best Local S
Matches
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 19839,
                                                                                                                                                                                                                                                                                                                                          APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (414) 271-3552
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION: APPLICANT: Ikuko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 599 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                               ORGANISM: Candida albicane
                                                                                                                        TYPE: PRT
                                      NAME/KEY: UNSURE LOCATION: (602)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Ryser, David G.
REGISTRATION NUMBER: 36,407
REFERENCE/DOCKET NUMBER: 65:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/O: FILING DATE: CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Milwaukee
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VENTION: CLONED NUCLEOTIDE PYROPHOSPHOHYDRALASE AND
VENTION: USES THEREOF
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FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 8459
LENGTH: 451
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8459
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Best Local Similarity
Thes 6; Conserve
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Search completed: November 29, 2005, 23:04:21
Job time : 30.6364 secs
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                                                                                                                                                                                                ; ORGANISM: Drosophila melanogaster US-09-270-767-58606
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US-09-270-767-58606
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                                                                                                                                                                                                                                           APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 58606
LENGTH: 55
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 58606, Application US/09270767 Patent No. 6703491 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION: APPLICANT: Gary Bro
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                                                                                                                                 Matches
                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                  TYPE: PRT
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Pred. No. 94;
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protein -9

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

November 29, 2005,

22:35:04 ; Search time 115.091 Seconds (without alignments)
73.562 Million cell updates/sec

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RESULT 2
QGEWH8 PIG
ID VGEWH8;
AC QGEWH8;
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DT 25-OCT-2004 (TIEMBLrel. 28, La
DT 26-OCT-2004 (TI
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ID QGEVH7;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
Oryctolagus.
NCBI_TaxID=9986;
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Strong R., Belsham G.J.;
"Sequential modification of translation initiation factor eIF4GI by two different foot-and-mouth disease virus proteases within infected BHK cells; identification of the 3Cpro cleavage site.";
J. Gen. Virol. 85:2953-2962(2004).
EMBL; AJ746224; CAG34104.1; -; mRNA.
100 TER 175 175
NON TER 175 NA; 19399 MW; C53979B9BA79CCCB CRC64;
                                                                                                                                                                     Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suida
      NUCLEOTIDE SEQUENCE.
PubMed=15448358; DOI=10.1099/vir.0.80254-0;
Strong R., Belsham G.J.;
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ive 0; Mismatches 0;
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Q58047 PYRHO
BMP3 RAT
Q59G53 HUMAN
Q4RFG9_TETING
Q91KQ7 ARATH
Q69S49_ORYSA
Q91K39 ARATH
Q76E23_ARATH
Q76E23_ARATH
Q75T0X9_HUMAN
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Minimum Maximum

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Scoring Sequence: Title: Perfect score:

table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

2166443 seqs,

705528306 residues

US-10-019-198A-1 64

KKRYDREFLLGF 12

Database

2::

UniProt\_05.80:\*
L: uniprot\_sprot:\*
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Result. Score Query Match Length 100.0 DB Q6EVH7 RABIT
Q6EVH6 PIG
Q6EVH0 HORSE
Q6EVI3 SHEEP
Q6EVI3 SHEEP
Q6EVI4 MESAU
Q6EVH9 MOUSE
IF4G1 RABIT
Q7YS39 FELCA
IF4G1 HUMAN
IF4G1\_MOUSE Q4T918\_TETING
Q6ZZ82\_SPHGR
Q6ZZ82\_SPHGR
Q6ZQYS\_MOUSE
IF4G3\_MOUSE
IF4G3\_MOUSE
CRYNE
Q5SZY6\_CRYNE
Q5SZY6\_CRYNE
Q5SZP9\_CRYNE
Q5SZP9\_CRYNE
Q5SZP9\_CRYNE
Q5SZP9\_CRYNE
Q5SZP9\_CRYNE
Q4T2D5\_TETING Q4LE59 HUMAN Q4RYZ6 TETNG Q5SMD1 HUMAN Q4R3V6 MACFA Q504Z1 HUMAN 1F4G3 HUMAN Q5SWC3 HUMAN Q6RZX2 HORSE Q59GJO HUMAN ij Q6evi3 Q6evi9 Q6evh9 P41110 Q7y837 Q074637 Q41258 Q41258 Q41258 Q413v6 Q58wd1 Q572x2 Q5672x2 Q5672x2 Q5672x2 Q572x2 Q572x Q6evh7 Q6evh8 Q6evi0 Q6evi2 Description 6 mus musculu 3 homo sapien homo sapien
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25-OCT-2004 (TremBLrel. 28, La
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EMBL; AJ7
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PubMed=1544358; DOI=10.1099/vir.0.80254-0;
Strong R., Belsham G.J.;
"Sequential modification of translation ini
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Strong R., Belsham G.J.;
"Sequential modification of translation initiation
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Name=eIF4GI;
                                                                                                                                Pecora; Bovidae;
NCBI_TaxID=9913;
                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Crani:
Mammalia; Eutheria; Laurasiatheria;
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Mammalla; Eutheria; Laurasiatheria;
MCBI_TaxID=9796;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25_PCT-2004 (TrEMBLrel. 28, Last annotation update)
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L; AJ746223; CAG34103.1; -; mRNA.
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Pred. No.
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Pred. No.
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neria; Cetartiodactyla;
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neria; Perissodactyla;
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Eukaryota; Metazoa; Chordata; Crania
Mammalia; Eutheria; Laurasiatheria;
Pecora; Bovidae; Caprinae; Ovis.
                  NUCLECTIDE SEQUENCE.
PubMed=15448358; DOI=10.1099/vir.0.80254-0;
Strong R., Belsham G.J.;
                                                                                             Eukaryota, Metazoa; Chordata; Crar
Mammalia; Eutheria; Euarchontoglii
Muridae; Cricetinae; Mesocricetus
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RESULT 7
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EMBL; AJ746220; CAG34100.1; -; mRNA.
NON_TER 1 1
NON_TER 175 175
SEQUENCE 175 AA; 19562 MW; 4E4FA
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SEQUENCE
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
EIF4GI protein (Fragment).
Name=Eif4GI; Synonyms=eIF4GI;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  two different foot-and-mouth disease virus proteases within infected BHK cells; identification of the 3Cpro cleavage site."; J. Gen. Virol. 85:2953-2962(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strong R., Belsham G.J.;
"Sequential modification of translation initiation factor eIF4GI
"Sequential modification of the sease virus proteases within infective different foot-and-mouth disease virus proteases within infective construction of the 3Cpro cleavage site.";

BHK cells; identification of the 3Cpro cleavage site.";

J. Gen. Virol. 85:2953-2962(2004).

EMBL; AJ46222; CAG34102.1; -; mRNA.

MGI; MGI:2384784; Eif4g1.
                                                                                                                                                                                                                     01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Eukaryotic translation initiation factor 4 ga
(eIF-4G1) (eIF-4G 1) (p220).
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurogna
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                                                                                                                                                Name=BIF4G1; Synonyms=EIF4G;
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata;
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PubMed=15448358; DOI=10.1099/vir.0.80254-0;
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P41110;
     NUCLEOTIDE
STRAIN-New
                                                                Oryctolagus.
NCBI_TaxID=9986;
                                                                                                                                             Eukaryota;
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175 AA;
SEQUENCE, AND PROTEIN SEQUENCE OF Zealand white; TISSUE-Brain;
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ilarity 100.0%;
Conservative 0
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19532 MW;
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Pred. No. 0.00061;
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RESULT 9
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Pfam; PF02854; MIF4G; 1.
Pfam; PF020200; WG; 1.
SMART; SM00515; GIF5C; 1.
SMART; SM00544; MA3; 1.
SMART; SM00544; MA3; 1.
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J. Biol. Chem. 267:2326-23231(1992). X

-i- FUNCTION: Component of the protein complex eIF4F, which is involved in the recognition of the mRUM cap, ATP-dependent unwinding of 5'-terminal secondary structure and recruitment of mRUM to the ribosome.

SUBUNIT: eIF4F is a multi-subunit complex, the composition of which varies with external and internal environmental conditions. It is composed of at least EIF4A, EIF4B and EIF4G1/EIF4G3. Interacts with eIF3, mutually exclusive with EIF4A1 or EIFA2, EIF4B and through its N-terminus with PAPBC1. Interacts through the C-terminus with the serine/threonine kinases MKNK1, and with MKNK2. Appears to act as a scaffold protein, holding these enzymes in place to phosphorylate EIF4E (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lamphear B.J., Yan R., Yang F., Waters D., Liebig H.-D., Kl Kuechler E., Skern T., Rhoads R.E.;
"Mapping the cleavage site in protein synthesis initiation 4 gamma of the 2A proteases from human Coxsackievirus and rhinovirus.";
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COMPBIAS
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J. Biol. Chem.
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SMR; P41110; 1036-1367
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MEDLINE=93054654; PubMed=1429670;
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InterPro; IPR003890; IF_eIF4G.
InterPro; IPR003891; IF_eIF4G_MA3
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Pred. No. 0.0054;
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Pfam; PF02847; MA3; 1.
Pfam; PF02854; MIF4G; i)
Pfam; PF02020; W2; 1.
SMART; SM00515; eIF5C;
SMART; SM00544; MA3; 1
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HSSP; 0434
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InterPro;
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                                                             "Human eukaryotic translation initiation two separate and independent binding site Mol. Cell. Biol. 17:6940-6947(1997).
                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM E), INTERACTION WITH EIF4A, AND MUTAGENESIS OF LEU-769; LEU-772; PHE-777; 843-LEU-LEU-844; 852-PHE-GLU-852; LEU-897; ILE-903; LEU-906; ARG-975; PHE-978; LEU-908; LEU-908; ARG-975; PHE-978; LEU-908; ARG-975; PHE-978; LEU-908; LEU-908; ARG-975; PHE-978; LEU-908; ARG-975; PHE-978; LEU-908; LEU-908; ARG-975; PHE-978; LEU-908; LEU-908; ARG-975; PHE-978; LEU-908; ARG-975; PHE-978; LEU-908; LEU-908; ARG-975; PHE-978; LEU-908; LEU-908; ARG-975; PHE-978; ARG-978; ARG-975; ARG-975; ARG-975; ARG-975; ARG-975; ARG-975; PHE-978; ARG-975; ARG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Brain;
MEDLINE=93054654; PubMed=1429670;
MEDLINE=93054654; PubMed=1429670; Rhoads R.
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER
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Mammalia; Eutheria;
                                                                                                                                                             Imataka H.,
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   NUCLEOTIDE
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P; 07YS39; 574-814.
GO:0003723; F:RNA binding; IEA.
GO:0003743; F:rranslation initiation factor activity;
GO:0003741; P:protein biosynthesis; IEA.
GO:0006442; P:protein biosynthesis; IEA.
GO:0006446; P:regulation of translational initiation;
GO:0006406; P:regulation of translational initiation;
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yota; Metazoa; Chordata;
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PF02854; MIF4G; 1.
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IPR003891; IF_eIF4G_MA3.
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                               267:23226-23231(1992)
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[MRNA] (ISOFORM B),
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Pred. No. 0.0054;
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heria; Carnivora; Fissipedia; Felidae;
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AND INTERACTION WITH
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eIF4A.";
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"Generation factor 4GI b
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                                                      NUCLEOTIDE SEQUENCE [MRNA] OF 30-206, NUCLEOTIDE DIA] OF 180-234, AND INTERACTION WITH ROTAVIRAL N PUBWed-9955181; DOI-10.1093/emboj/17.19.5811; Piron M., Vende P., Cohen J., Poncet D.; Procet D.; Rotavirus RNA binding protein NSP3, interacts withe poly(A) binding protein from eIF4F."; pmp0 J. 17:5811-5821(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22048027; PubMed=12052860;
DOI=10.1128/MCB.22.13.4499-4511.2002;
Byrd M.P., Zamora M., Lloyd R.E.;
NUCLEOTIDE SEQUENCE OF 604-722, I MUTAGENESIS OF TYR-612 AND 617-LE MEDLINE=95379845; PubMed=7651417;
                                                                                                                                                                          The German cDNA consortium; Submitted (JAN-2005) to the
                                                                                                                                                                                                       TISSUE=Endometrial tumor;
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Ota T., Suzuki Y., Nishikawa T., Ots
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NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA]
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"A newly identified N-terminal a
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            AND 617-LEU-LEU-618.
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INTERACTIONS WITH EIF4E AND EIF4EBP1.
MEDLINE=96091142; PubMed=8521827;
Haghighat A., Mader S., Pause A., Son
"Repression of cap-dependent translat:
competition with p220 for binding to 4E.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MUTAGENESIS OF GLY-682.
MEDINE=97121269; PubMed=8961935; DOI=10.1021/bi961864t;
Lamphear B.J., Rhoads R.E.;
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Nature 371:762-767(1994).
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"The translation initiation factor elf-4E binds to a common motif
shared by the translation factor elf-4 gamma and the translational
repressors 4E-binding proteins.;
repressors 1E-binding proteins.;
Col. Cell. Biol. 15:4990-4997(1995).
                                                                                                                                                                                                                                                                                                                                                                                     Gingras A.-C., Raught B., Sone "eIF4 initiation factors: effe and regulators of translation. Annu. Rev. Blochem. 68:913-963
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                                                                                                                     INTERACTION WITH MKNK2.

PubMed=11154262; DOI=10.1128/MCB.21.3.743-754.2001;

PubMed=11154262; DOI=10.1128/MCB.21.3.743-754.2001;

Scheper G.C., Morrice N.A., Kleijn M., Proud C.G.;

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"Is a eukaryotic initiation factor 4E kinase with high levels of basa:

activity in mammalian cells.";

Mol. Cell. Biol. 21:743-754 (2001).
PubMed=15302935; DOI=10.1073/pnas.0404720101; Beausoleil S.A., Jedrychowski M., Schwartz D., Elias J.E., Villen J. J., Cohn M.A., Cantley L.C., Gygi S.P., Cohn M.A., Cantley L.C., Gygi S.P., "Large-scale characterization of HeLa cell nuclear phosphoproteins. Proc. Natl. Acad. Sci. U.S.A. 101:12130-12135(2004).
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MEDLINE-99094911; PubMed-9878069; DOI=10.1093/emboj/18.1.270;
MEDLINE-99094911; PubMed-9878069; DOI=10.1093/emboj/18.1.270;
                                                                                                                                                                                                                                                    "Human eukaryotic translation initiation mnk1 to phosphorylate eIF4E."; EMBO J. 18:270-279(1999).
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                                                                                       PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                       Sonenberg N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            iochemistry 35:15726-15733(1996).
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translation by 4E-binding protein 1:
nding to eukaryotic initiation factor-
                                                                                                                                                                                                                                                                                                                                                                                                                            of mRNA
                                                                                                                                                                                                                                                                                          factor 4G
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RESULT 11
IF4G1_MOUSE
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                                                                               RP NUCLEOTIDE SEQUENCE [LARGE SCALE WENNA] (ISOFORMS 1 AND 2).

RC STRAIN=C57BL/6; TISSUE=Brain, and Fetal brain;

RC STRAIN=C57BL/6; TISSUE=Brain, and Fetal brain;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX MISCALLAN, Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Bettow K.J., Wang J., Hong L.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramon R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulty S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulty S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulty S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulty S.W.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Butkesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Butkesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Butkesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Butkesley R.W., Touchman J.W., Schmutz J., Myers R.M.,

RGeneration and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences ",

Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
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Matches 12
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Bellsolell L., Cho-Park P.F., Poulin F., Sonenberg N., Burley S.F.
"Two HEAT domains in the C-terminal portion of human EIF4G suppor
binding to EIF4A and MNK1.";
Submitted (MAR-2005) to the PDB data bank.
-i- FUNCTION: Component of the protein complex eIF4F, which is
involved in the recognition of the mRNA cap, ATP-dependent
unwinding of 5'-terminal secondary structure and recruitment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [19]
X-RAY CRYSTALLOGRAPHY (2.38 ANGSTROMS)
ROTAVIRAL NSP3, INTERACTION WITH PABP,
ILE-182; ILE-192 AND ILE-196.
ILE-182; ILE-197 AND ILE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Groft C.M., Burley S.I "Recognition of eIF4G circularization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ĪF4G1 MOUSE STANDARD; PRT; 1600 AA. Q6NZJĞ; Q6NZNB; Q8BW99; 13-SEP-2005 (Rel. 48, Last sequence update) 13-SEP-2005 (Rel. 48, Last annotation update) 13-SEP-2005 (Rel. 48, Last annotation date) Eukaryotic translation initiation factor 4 gar
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PubMed=12086624; DOI=10.1016/S1097-2765(02)00555.
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Muroidea; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
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Mammalia; Eutheria; Euarchontoglires; Glires;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
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STRAIN=C57BL/6J;
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                             NUCLEOTIDE SEQUENCE
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SUBUNIT: eIF4F is a multi-subunit
which varies with external and int
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ilarity 100.0%;
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lires; Rodentia; Sciurogna
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A Birney E., Hayashizaki Y.;

RT GO,770 full-length cDNAs.";

RI GO,770 full-length cDNAs.";

RI Wature 420:653-573 (2002).

CC --- FUNCTION: Component of the protein complex eIF4F, which is involved in the recognition of the mRNA cap, ATP-dependent unwinding of 5'-terminal secondary structure and recruitment of CC mRNA to the ribosome (By similarity).

CC --- SUBUNIT: eIF4F is a multi-subunit complex, the composition of CC which varies with external and internal environmental conditions.

CC It is composed of at least EIF4A, EIF4E and EIF4G1/EIF4G3.

CC IT is composed of at least EIF4A, EIF4E and EIF4G1/EIF4G3.

CC EIF4E and through its N-terminus with PAPBC1. Interacts through CC its C-terminus with the serine/threonine kinases MKNK1, and with GC its C-terminus with the serine/threonine kinases MKNK1, and with GC in place to phosphorylate EIF4E. Non-phosphorylated EIF4E; insulin CC stimulated MAP kinase (MAPK1 and MAPK3) phosphorylation of EIF4G1/EIF4G3 to interact with EIF4E; insulin GC stimulated mAP kinase (MAPK1 and MAPK3) phosphorylation of EIF4G1/EIF4G3 to bind and consequent initiation of translation (By similarity).
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RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kiyosawa H.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
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RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
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RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
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RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I.,
RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
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RA Minaka E., Jakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Miraya E., Hawashizawa M., Waterston R., Lander B.S., Rogers J.,
RA Miraya E., Hawashizawa M., Waterston R., Lander B.S., Rogers J.,
RA Marney E., Hawashizawa M., Waterston R., Lander B.S., Rogers J.,
RA Marney E., Hawashizawa M., Waterston R., Lander B.S., Rogers J.,
MGI; MGI:2384784; Eif4g1.
GO; GO:0005737; C:cycoplasm; IDA.
GO: GO:005737; C:cycoplasm; IDA.
InterPro; IPR003390; IF_GIF4G.
InterPro; IPR003891; IF_GIF4G_MA3.
                                                                                                                                                                                                                                                                                                          EMBL; BC066038; AAH66038.1; -; mRNA.

EMBL; BC066103; AAH66103.1; -; mRNA.

EMBL; BC09675; AAH79675.1; -; mRNA.

EMBL; BC09674; BAC3582.1; -; mRNA.

EMBL; AK053144; BAC3582.1; -; mRNA.

SMR; Q6NZJ6; 755-995, 1234-1565.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to bind and consequent initiation ALTERNATIVE PRODUCTS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=Q6NZJ6-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IBOId=Q6NZJ6-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       long as its content is in no way modified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence=VSP_013974, VSP_013975; gs to the eIF4G family.
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RESULT 13
Q4RYZ6_TETNG
ID Q4RYZ6_T
AC Q4RYZ6;
DT 13-SEP-2
DT 13-SEP-2
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Q4LE58 HUMAN F
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MOD_RES
MOD_RES
Qqryz6 TETNG PRELIMINARY;
Qqryz6;
13-SEP-2005 (TrEMBLrel. 3:
13-SEP-2005 (TrEMBLrel. 3:
                                                                                                                                                                                                                 Nakajima D., Saito K., Yamakawa H., Kikuno R.F., Nakayama M., Ohara R., Okazaki N., Koga H., Nagase T., Ohara O., "Preparation of a set of expression-ready clones of mammalian cDNAs encoding large proteins by the ORF trap cloning method." Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
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SMART; SM00544; MA3; 1.
SMART; SM00544; MA3; 1.
Alternative splicing; Initiation factor; Phosphorylation;
Alternative splicing; RNA-binding; Translation regulation
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
EIF4G1 variant protein (Fragment).
Name=EIF4G1 variant protein;
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                                                                                                                                                                                                                                                                         TISSUE=Brain;
                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria;
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Pfam; PF02020; W2; 1.
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12; Conserv
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eIF3/EIF4A-binding (By similarity).
EIF4A-binding (By similarity).
Necessary but not sufficient for MKNK1-
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Phosphoserine (By similarity).
Missing (in isoform 2).
/FTId=Vsp 013974.
Missing (In isoform 2).
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                                                                                                                                   Score 64; DB 2; Pred. No. 0.0062;
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Asp/Glu-rich.
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W; 8664A8B449C7A128 CRC64;
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                                   PRT;
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RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Micaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Neilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Crusud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Crusud C., Luprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Falls M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
RA Kills M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate protc-karyotype.";
RN Nature 431:946-957(2004).
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Best Local S
Matches 11
Bird C.;
Submitted (MAY-2005) to the E
EMBL; AL666477; CAI12535.1; -
EMBL; AL358392; CAI12158.1; -
EMBL; AL358392; CAI12535.1; J
EMBL; AL606477; CAI12158.1; J
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Chromosome 16 (Fragment).
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Eukaryota; Metazoa; Chordata; Craniara; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q5SWD1;
01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Eukaryotic translation initiation factor 4 gamma, 3
Names-EIF4G3; ORFNames-RP11-190H11.1-007;
Homo sapiens (Human)
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                            Tracey A.
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HUMAN
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Search completed: November 29, Job time : 118.091 secs

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RP NUCLEOTI RA Internat RA "Internat RA "DNA segg RT evolutio RL Submitte RN QS SEQUENCE RI Submitte RN Sugano SRT "Submitte RA Sugano SRT "Submitte RA Sugano SRT "Submitte RT Comparat RL Submitte RI Sub
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Matches 10
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last samotation update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Testis cDNA clone: QteA-13802, similar to human eukaryotic translation factor 4 gamma, 3(EIF4G3),
Macaca fascicularis (Crab eating macace) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecidae; Cercopithecinae; Macaca.
MCBI TaxID=9541;
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SEQUENCE 247 AA; 27753 MW; AA6C465E14F6232C CRC64;
                                                                                                                                                                                                                                                                                    Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y., Sugano S., Gojobori T., Shen J.C.-K., Wu C.I., Hashimoto K.; "Substitution rate and structural divergence of 5'UTR evolution: Comparative analysis between human and cynomolgus monkey cDNAs."; Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          International consortium for macaque cDNA "DNA sequences of macaque genes expressed evolutionary implications.";
Submitted (JUN-2005) to the EMBL/GenBank/I
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KKOYDREFLLDF
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## ALIGNMENTS

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translation initiation factor eIF4-gamma - rabbit C;Species: Oryctolagus cuniculus (domestic rabbit) C;Species: Oryctolagus cuniculus (domestic rabbit) C;C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004 C;Accession: I46707 R;Yan, R: He, W: Rhoads, R.E.
J. Biol. Chem. 268, 19200-19203, 1993 A;Title: Mapping the Cleavage site in protein synthesis initiation factor eIF-4 gamma of A;Title: Mapping the Cleavage site in protein synthesis initiation factor eIF-4 gamma of A;Accession: I46707; MUID:93374895; PMID:8396129 A;Accession: I46707; MUID:93374895; PMID:8396129 A;Accession: I46707
A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A,Residues: 1-1402 <YAN>
A;Cross-references: UNIPROT:P41110; UNIPARC:UPI000012D372; GB:L22090; NID:9404774; PIDM:
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J. Biol. Chem. 267, 23226-23231, 1992
A;Title: Amino acid sequence of the human protein synthesis initiation factor eIF-4 gamma A;Reference number: A44453; MUID:93054654; PMID:1429670
A;Accession: A44453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           translation initiation factor eIF-4 gamma - human C;Species: Homo sapiens (man) C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 08-Dec-1994 C;Accession: A44453
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A;Residues: 1-1396 cYAN>
A;Cross-references: UNIPARC:UPI000017C3F3
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIP:118286)
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C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_Change varuation.
C;Accession: B64622
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
                                          R;Kawarabayasi, Y.; Sawada, M.;
M.; Ohfuku, Y.; Funahashi, T.;
DNA Res. 5, 55-76, 192
A;Title: Complete sequence and g
A;Reference number: A71000; MUID
A;Accession: G71456
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A; Gene:
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C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004
C;Accession: G71456
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A;Residues:
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C;Species: Pyrococcus horikoshii
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                                                            and gene organization of the ; MUID:98344137; PMID:9679194
                           acid sequence not shown;
                                                                                                          Horikawa, H.; Haikawa, Y.; Hino, Tanaka, T.; Kudoh, Y.; Yamazaki,
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J.; Kushida,
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translation initiation factor eIF-4 gamma homolog F27H5.30 [similarity] - A (Alternate names: protein F27H5.30 (similarity] - A (C)Species: Arabidopsis thaliana (mouse-ear cress) (C)Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004 (C)Accession: T49219
                                                                                                                                                                                                                                                                         R;Rieger, M.; Mueller-Auer, S.;
submitted to the Protein Sequend
A;Reference number: Z25018
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A;Residues: 1-360 <RES>
A;Cross-references: UNIPARC:UPI0000170CBA; GB:S77492; NID:g957225;
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R;Chen, D.; Feng, J.Q.; Feng, M.; Harris, M.A.; Mahy, P.; Mundy, DNA Cell Biol. 14, 235-239, 1995
A;Title: Sequence and expression of bone morphogenetic protein 3 A;Reference number: I53032; MUID:95186061; PMID:7880444
A;Accession: I53032
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A;Note: this accession replaces an interim accession for a sequence replaced by GenBank C;Genetics:
A;Gene: PH0309
                                                                                                                   A;Map position: 3
A;Introns: 455/3; 1370/2; 1435/2; 1523/1; 1529/1; 1558/3; 1586/2
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C;Superfamily: inhil
                                                                                                                                                    A; Gene: ATSP: F27H5.30
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e, April 2000
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RESULT 9
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R;Van Sloun, P.P.H.; Romeijn, R.J.; Beken, J.C.J
Mutat. Res. 433, 109-116, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA-directed DNA polymerase (EC 2.7.7.7) zeta chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                   C;Accession: T09072
R;Hernandez, G.; Castellano, M.M.; Agudo, M.; Sierra, J.M. Eur. J. Biochem. 253, 27-35, 1998
A;Title: Isolation and characterization of the cDNA and the A;Reference number: Z16553; MUID:98237569; PMID:9578457
A;Accession: T09072
                                                                                                                                                                                                                             probable translation initiation factor eIF-4 gamma - fruit fly (Drosophila melanogaster) N;Alternate names: translation initiation factor eIF4G C;Species: Drosophila melanogaster C;Species: Drosophila melanogaster C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004 C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
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A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A33650; MUID:20512582; PMID:11058132
A;Accession: G83933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dipaptidase BH2271 [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004 C;Accession: G83933
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C;Keywords: nucleotidyltransferase
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A;Residues: 1-3122 <VAN>
A;Cresidues: 1-3122 <VAN>
A;Cross-references: UNIPROT:Q61493; UNIPARC:UPI0000028721; EMBL:AF083464; NID:g4079830;
A;Experimental source: strain 129/Ola; testis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source: strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:Q9KAL6; UNIPARC:UPI00000C3E6A; GB:AP001515; GB:BA000004; NII
A;Experimental source: strain C-125
    A;Residues: 1-1666 <HER>
A;Cross-references: UNIPROT;O61380; UNIPARC:UPI000007DECF; EMBL:AF030155; NID:g3056722;
                                                           A; Molecule type: mRNA
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                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
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source: strain Oregon
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A;Molecule type: DNA
A;Residues: 1-1418 <POH>
A;Experimental source: strain S288C
A;Experimental source: strain S288C
A;Experimental source: strain S288C
A;Banes, V.; Rechmann, S.; Nentwich, U.; Schwager, C.; Ansorge, W.; Voss, H.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S64920
A;Accession: S64920
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A;Map position: 4
C;Keywords: protein biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the Protein Sequence Database, May 1990 A;Reference number: S64899 A;Accession: S64918
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                                                             A; Map position:
C; Superfamily: c
                                                                                  A;Cross-references: SGD:S0004076
A;Map position: 12R
                                                                                                                                                                    A; Molecule type: DNA A; Rotlecule type: DNA A; Residues: 257-1418 <BEN> A; Residues: 257-1418 <BEN> A; Cross-references: UNIPARC: UPI0000168F70; EMBL: 273258; MIPS: YLR086w A; Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Saccharomyces cerevisiae C;Date: 01-Aug-1995 #sequence_revis C;Accession: S64918; S64920
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A; Residues: 1-332 < RES>
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A;Title: The DNA sequence and minimal replicon of the Corynebacterium glutamicum plasmid
A;Reference number: I40726; MUID:94014972; PMID:8409918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Archer, J.A.; Sinskey, A.J.
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                                                             Superfamily: chromosome
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58.6%;
66.7%;
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Pred. No.
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Pred.
Score 37.5;
Pred. No. 1.
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5; DB 2;
1.1e+02;
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prolyl-tRNA synthetase NMB1339 [imported] - Neisseria meningitidis (strain MC58 serogrou
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: C81094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A;Reference number: A72450; MUID:99310339; PMID:10382966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein APE1495 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 05-Oct-2004
C;Accession: G72629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, ; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Haemophi
C;Date: 18-Aug-1995
C;Accession: D64133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary A;Molecule type: DNA
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C;Superfamily: probable alkaline phosphatase yngC
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A; Residues: 1-212 <TIGR>
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                                                                                                              RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein HI1629 - Haemophilus influenzae (strain Rd KW20)
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A;Molecule type: DNA
A;Residues: 1-570 <TET>
A;Residues: 1-570 <TET>
A;Cross-references: UNIPROT:Q9JZ14; UNIPARC:UPI00000C46B1;
A;Experimental source: serogroup B, strain MC58
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                  R;Tettelin, H.; Saunders, N.J.; Heidelberg; J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.Å. Hickey, B.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000

A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Vet A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

A;Reference number: A81000; MUID:20175755; PMID:10710307
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                                                                                                                                                                       A;Gene: NMB1339
C;Superfamily: |
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A; Status: preliminary
                                                                                  Matches
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                                         1 KKRYDREFLLG 11
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KDRHDRDFCMG
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107
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                                                                                                         Score 37;
Pred. No.
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Search completed: November 29, 2005, 23:02:30 Job time: 20.8182 secs

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Minimum
Maximum
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Maximum Match 100%
Listing first 45 summaries
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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seq length: 2000000000
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6: geneseqp2003
7: geneseqp2003
8: geneseqp2003
9: geneseqp2003
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Match
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Gapop 10.0 , Gapext 0.5
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64
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AAB11096
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46.030 Million cell updates/sec
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Aab11100 Zebrafish
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Aab31438 A human
Aab31450 Peptide
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    The human

7 Human eIF

7 Hebindin

8 Human adi

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38	39	39	39	39	39	39	39	40	40	40	40	40	40	40	40	42	44	44	45	
59.4	•	•	60.9	60.9	60.9	60.9	60.9	62.5	62.5	62.5	62.5	62.5	62.5	62.5	62.5	65.6	68.8	68.8	70.3	75.0
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AAY59752	ABB72054	ADB10592	ADB10594	ADB10596	ADS28271	AAB84406	AAB11101	ADE09353	ADE09433	ADX07307	ADR46703	ADR15681	ADK40962	ADC54131	ADI45381	ABM86083	AAW20906	AAW20422	AAB31451	ADQ97959
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# RESULT 1 AAB31445 AAB31445 standard; peptide; 12 AA. AAB31445;

ALIGNMENTS

Peptide derived from human eukaryotic Initiation Factor 4G (eIF4G). 20-APR-2001 (first entry)

Binding peptide; eukaryotic Initiation Factor 4G; eIF4G; eIF4E; cell death; cell apoptosis; anticancer; antitumor.

Homo sapiens.

WO200078803-A2.

28-DEC-2000.

21-JUN-2000; 2000WO-GB002414.

21-JUN-1999; 99GB-00014480

(UYDU-) UNIV DUNDEE.

Proud CG, Herbert TP, Lane DP, Fahraeus

WPI; 2001-071386/08.

Use of eukaryotic Initiation Factor 4E (elF4E) binding agents e.g. elF4E-binding peptide (elF4E-BP) derivatives as anticancer or antitumor agents for inducing apoptosis in e.g. mammalian tumor cells.

Example; Fig 5; 46pp; English.

The present sequence represents a peptide derived from an eukaryotic Initiation Factor 4G (eIF4G) protein. The specification describes elf and eIF4E binding agents, such as peptides or peptidemimetics. These binding agents are used for the induction of cell death. The binding peptides are used for inducing cell apoptosis. They are used in pharmaceutical compositions for anticancer or antitumor treatment of mammalian cells. Specifically, the peptides result in growth inhibitiof, or increased cytotoxicity to tumour cells inhibition eIF4G

Sequence 12 AA;

100.0%; Score 64; 멂

4

Length 12;

Query Match

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RESULT 3
AAB31450
ID AAB3
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AC AAB3
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Best Local
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                                                                                                                                                                                                                The present sequence represents a binding peptide for an eukaryotic Initiation factor 4G (eIF4G) protein. The specification describes eIF4G and eIF4E binding agents, such as peptides or peptidemimetics. These binding agents are used for the induction of cell death. The binding peptides are used for inducing cell apoptosis. They are used in pharmaceutical compositions for anticancer or antitumor treatment of mammalian cells. Specifically, the peptides result in growth inhibition of, or increased cytotoxicity to tumour cells
                                                                                                                                                                                                 Sequence 12
                                                                                                                                                                                                                                                                                                                         Use of eukaryotic Initiation Factor 4E (elF4E) binding agents e.g. elF4E-binding peptide (elF4E-BP) derivatives as anticancer or antitumor agents for inducing apoptosis in e.g. mammalian tumor cells.
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cell death; cell
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            Peptide derived from human
                                                                     AAB31450 standard; peptide; 14 AA
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                               20-APR-2001
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12; Conserv
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            eukaryotic
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anticancer; antitumor.
                                                                                                                                                        Score 64; DB 4; Pred. No. 9.7e-05;
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             Initiation
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           Factor
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            4G
            (eIF4G)
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                                                                               19-OCT-2000
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                                                                                                                   Homo sapiens.
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The present sequence represents a peptide derived from an eukaryotic Initiation Pactor 4G (e1F4G) protein. The specification describes eIF4G and eIF4E binding agents, such as peptides or peptidemimetics. These binding agents are used for the induction of cell death. The binding peptides are used for inducing cell apoptosis. They are used in pharmaceutical compositions for anticancer or antitumor treatment of mammalian cells. Specifically, the peptides result in growth inhibition of, or increased cytotoxicity to tumour cells. note: the peptide is biotinylated and linked to penetratin
                                                                                                                                                                                                                                                                                                                        Eukaryotic initiation factor; eIF4E; transgenic animal; antidiabetic; knockout mutation; 4E-BP1; glucose metabolism; fat metabolism; anorec drug; anti-obesity; anti-fat deposition; anti-metabolic.
09-APR-1999; 99US-0128559P.
02-FEB-2000; 2000US-0179743P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB11096 standard; peptide; 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Use of eukaryotic Initiation Factor 4E (elF4E) binding agents e.g. elF4E-binding peptide (elF4E-BP) derivatives as anticancer or antitumor agents for inducing apoptosis in e.g. mammalian tumor cells.
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                                                                                  07-APR-2000; 2000WO-CA000388
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Pred. No.
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RESULT 5
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Best Local
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16-FEB-2001
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Non-human transgenic animal useful as model for studying lipid and glucose metabolism, has germ and somatic cells containing knockout mutation in DNA encoding eukaryotic initiation factor 4E-binding pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryotic initiation factor; eIF4E; transgenic animal; antidiabetic; knockout mutation; 4E-BP1; glucose metabolism; fat metabolism; anorectic; drug; anti-obesity; anti-fat deposition; anti-metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB11100 standard;
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02-FEB-2000; 2000US-0179743P.
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                                                                                                                                          Sonenberg N,
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Pred. No. 0.00013;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel non-human transgenic animal (I) whose germ cells and somatic cells contain a knockout mutation in DNA encoding a 48-BP1 (a member of eukaryotic initiation factor 4E (eIF-4E)-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryotic initiation factor; eIF4E; transgenic animal; antidiabetic; knockout mutation; 4E-BP1; glucose metabolism; fat metabolism; anorec drug; anti-obesity; anti-fat deposition; anti-metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rabbit eIF-4E recognition motif peptide heIF4GI.
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                                                                                                              Non-human transgenic animal useful as model for studying lipid and glucose metabolism, has germ and somatic cells containing knockout mutation in DNA encoding eukaryotic initiation factor 4E-binding protein
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02-FEB-2000;
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                                                            Disclosure; Fig 7; 80pp; English
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This invention of germ cells and of a 4E-BP1 (a mem)

ion describes a novel non-human transgenic animal (I) whose and somatic cells contain a knockout mutation in DNA encoding member of eukaryotic initiation factor 4E (eIF-4E)-binding

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AAB84401-15 represent 4E-binding sites. 4E-binding protein 1 (4E-BP1) is a repressor of cap-dependent translation initiation, and selectively activates apoptosis in Ras-transformed fibroblasts and eliminates Ras-induced chemoresistance. The effects of 4E-BP1 are strictly dependent on its ability to sequester the translation initiation factor elf4E, thereby preventing its assembly into an active pre-initiation complex. The specification describes a method for inducing apoptosis in a cell in which the apoptosis pathway is inhibited. The method comprises decreasing the amount of elf4F pre-initiation complex by sequestration of elf4E, thus relieving an apoptosis block. The method is useful for modulating
                                                                                                                                                                                                                                                         Inducing apoptosis in useful for treating cadecreasing the amount apoptosis block.
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                                                       AABB4401-15 represent 4E-binding sites. 4E-binding protein 1 (4E-BP1) is a repressor of cap-dependent translation initiation, and selectively activates apoptosis in Ras-transformed fibroblasts and eliminates Ras-induced chemoresistance. The effects of 4E-BP1 are strictly dependent on its ability to sequester the translation initiation factor elf4E, thereby preventing its assembly into an active pre-initiation complex. The specification describes a method for inducing apoptosis in a cell in which the apoptosis pathway is inhibited. The method comprises decreasing the amount of elf4F pre-initiation complex by sequestration of elf4E, thus relieving an apoptosis block. The method is useful for modulating pro-apoptotic and anti-apoptotic pathways in cells, especially in Rastransformed cells. Thus, the method aparticularly useful for treating cancer. The elf4E sequestering agent, 4E-BP1 or its elf4E binding portion is useful for treating high proliferative cells
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; 1
0.00013;
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                                                                                                                                        AABB4401-15 represent 4E-binding sites. 4E-binding protein 1 (4E-BP1) is a repressor of cap-dependent translation initiation, and selectively cactivates apoptosis in Ras-transformed fibroblasts and eliminates Ras-induced chemoresistance. The effects of 4E-BP1 are strictly dependent on its ability to sequester the translation initiation factor elf4E, thereby preventing its assembly into an active pre-initiation complex. The specification describes a method for inducing apoptosis in a cell in specification describes a method for inducing apoptosis in a cell in which the apoptosis pathway is inhibited. The method comprises decreasing the amount of elf4F pre-initiation complex by sequestration of elf4E, thus relieving an apoptosis block. The method is useful for modulating pro-apoptotic and anti-apoptotic pathways in cells, especially in Ras-transformed cells. Thus, the method is particularly useful for treating cancer. The elf4E sequestering agent, 4E-BP1 or its elf4E binding portion is useful for treating high proliferative cells
                                                         Query Match
Best Local S
Matches 12
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Matches 1
                                                                                                                                                                                                                                                                                                                                                                                                                  Inducing apoptosis in a cell in which the apoptosis pathway is inhibited, useful for treating cancer or highly proliferative cells, comprises decreasing the amount of elf4F pre-initiation complex, relieving an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MINU )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4E-binding site; 4E-binding protein; 4E-BP; 4E-BP1; chemor cap-dependent translation initiation repressor; apoptosis; translation initiation factor; elF4E; Ras; cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sonenberg N,
                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 6;
                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                       apoptosis block.
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UNIV MINNESOTA.
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12, Conserv
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                                                                                                                    16
                          KKRYDREFLLGF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   site of a elF4GI protein.
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ilarity 100.0%;
Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                           80pp;
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                                                                       Score 64; DB 4;
Pred. No. 0.00013;
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                                                            Mismatches
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                                                                                       Length 16;
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                                                            Indels
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RESULT 10

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ADR10076
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Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a peptide derived from an eukaryotic Initiation Factor 4G (eIF4G) protein. The specification describes eIF4G and eIF4E binding agents, such as peptides or peptidemimetics. These binding agents are used for the induction of cell death. The binding peptides are used for inducing cell apoptosis. They are used in pharmaceutical compositions for anticancer or antitumor treatment of mammalian cells. Specifically, the peptides result in growth inhibition of, or increased cytotoxicity to tumour cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Use of eukaryotic Initiation Factor 4E (elF4E) binding agents e.g. elF4E-binding peptide (elF4E-BP) derivatives as anticancer or antitumor agents for inducing apoptosis in e.g. mammalian tumor cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Binding peptide;
cell death; cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide derived from human eukaryotic Initiation Factor 4G (eIF4G).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 30 AA;
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                                                                                                                                   human; oligo-capping method; diagnostic marker; gene therapy; osteoporosis; neurological disease; Alzheimer's disease; Parkinson's disease; dementia; short memory; cancer; sense or motor function; emotional reaction; fear response; p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-071386/08
                                                                                                        osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
                                                                                                                                                                                                                                                                                                                                                  04-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADR10076 standard;
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                             Homo sapiens
                                                                                   tranquiliser.
                                                                                                                                                                                                                                                                                         Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein; 903 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                      for treating neurological disease Seq 3582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lane DP,
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Pred. No. 0.00025;
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention relates to novel, isolated full length human cDNA complexities and the encoded proteins thereof. Specifically, it refers to convert the encoded proteins thereof. Specifically, it refers to convert the encoded proteins thereof. Specifically, it refers to convert the encoded by an oligo-capping method, where none of these colones are identical to any known human mRNAs. The present invention converted to any known human mRNAs. The present invention converted to any known human mRNAs. The present invention converted to any known human mRNAs. The present invention converted to any known human mRNAs. The present invention as well as the used to bind to any known the cDNA molecules as such, these converted to any known the cDNA molecules. As such, these for the various diseases or morbid states. In particular, they are useful in the various disease or morbid states. In particular, they are useful in the therapy for treating osteoporosis, neurological disease, Alzhaimer's converted the sequence of sense or motor function, and they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian, constant and tranquiliser activities. This polypeptide is a protein encoded by a full length human cDNA sequence of the invention. NOTE: This sequence is not given in the sequence listing of the specification but office, because of the specification but office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local
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09-MAY-2003;
                                                     WO2003016475-A2
                                                                                     Homo sapiens
                                                                                                                                                             Human;
                                                                                                                                                                                                                                   29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 3582; 2686pp;
                    27-FEB-2003
                                                                                                                                          spinal
                                                                                                                                                                                              Human Protein Q04637, SEQ ID NO 11719.
                                                                                                                                                                                                                                                                    ADD46044;
                                                                                                                                                                                                                                                                                                  ADD46044 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New 1995 cDNA, useful
Alzheimer's diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-583265/57.
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                                                                                                                                          pain; neuronal tissue; gene therapy;
segmental nerve injury; chronic cons
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A, Ishii
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2003JP-00131452.
                                                                                                                        injury; SNI; Chung.
                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for treating osteoporosis, neurological diseases, Parkinson's diseases, dementia and various cancer
                                                                                                                                        injury; chronic constriction injury; CCI;
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                                                                                                                                                                                                                                                                                                       1395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 64; DB 8; Length 903; Pred. No. 0.0083;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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e R;
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that is differentially expressed in neuronal tissue of a first animal considered to pain, a method for identifying a compound which regulates the expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a cc method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the cs specification, a method for identifying a compound useful in treating cs pain and a pharmaceutical composition composition the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating capin (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene the sequence presented is a human protein (shown in Table 2 of the sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention discloses a composition comprising two or more isolated rat or human polynuclectides or a polynuclectide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence
                                                Sequence 1395 AA;
                                                                                       specification, but was obtained in electr
ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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BAYER AG.
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Length 1395;
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            S
                           Matches
                                 Local
413
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12; Conser
             1 KKRYDREFLLGF 12
KKRYDREFLLGF 424
                           Conservative
                                 100.0%;
                           0,
                                 Score 64;
Pred. No.
                           Mismatches
                                 DB 7;
                           0,
                           Indels
                           0
                           Gaps
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ADO19635 standard;

protein; 1396 AA

12-AUG-2004 (first entry)

ADO19635

PRO polypeptide #282.

RESULT 13
ADO19635
ID ADO19
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AC ADO19
XC ADO19
DT 12-AU
XX
DE Humar
XX
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KW Humar
KW Theun
KW Syste
KW autoi
KW autoi
KW diabe Human; PRO; immune related disorder; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis; systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis; autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroi diabetes mellitus; renal disease; demyelinating thyroiditis;

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ADP54731
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Best Local
                                        human; PRO; immune related disease; inflammatory immune response; immune response stimulation; antiallergic; antianaemic; antiarthritic; antiasthmatic; antidiabetic; antiinflammatory; antipsoriatic; antithyroid; CNS; dermatological; gastrointestinal; haemostatic; hepatotropic; immunostimulant; immunosuppressive; muscular; nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic; virucide; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to human PRO polypeptides and the polynucleotides encoding them. The polypeptides and polynucleotides are useful for treating and diagnosing immune related disorders in mammals. The immune related disorders in mammals the immune related disorders in clude systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, systemic sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune haemolyric anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central or peripheral nervous system, demyelinating polyneuropathy, Guillain-Barre syndrome and chronic inflammatory demyelinating polyneuropathy. This sequence represents a human PRO polypeptide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fong
Wood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                central nervous system; peripheral nervous system; demyelinating polyneuropathy; Guillain-Barre syndrome; chronic inflammatory demyelinating polyneuropathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for treating an immune related disorder such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
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N-PSDB; ADO19634.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1396 AA;
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                                                                                                                                                                       Human PRO protein sequence SEQ ID NO:707.
                                                                                                                                                                                                        18-NOV-2004 (first entry)
                                                                                                                                                                                                                                                                      ADP54731 standard; protein; 1396 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                  12; Conservative
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Wu TD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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Pred. No.
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RESULT 15 AAB18792

AAB18792 standard; protein; 1560 AA

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413

Query Match Best Local : Matches

Similarity

100.0%; Score 64; DB 8; Length 1396; 100.0%; Pred. No. 0.013;

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Conservative

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Mismatches

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Gaps

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KKRYDREFLLGF 12 KKRYDREFLLGF 424

Sequence 1396 AA;

**EXEXEXEX** 

22-JAN-2001 AAB18792;

(first

entry)

Human; ribosome recruitment protein; eIF4G1; RNA-binding protein;

recruitment protein eIF4G1

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The present invention describes an isolated PRO nucleic acid (I). Also clearibed: (I) a vector comprising (I); (2) a host cell comprising the creator of (I); (3) a process for producing a PRO polypeptides; (4) an cisolated PRO polypeptide; (5) a chimeric molecule comprising the composition of polypeptide; (5) a chimeric molecule comprising the composition of matter comprising a polypeptide of (4); (7) a composition of matter comprising a polypeptide of (4), an agonist or composition of the polypeptide or an antibody that binds to the polypeptide in combination with a carrier; (8) an article of manufacture polypeptide in combination with a carrier; (8) an article of manufacture comprising a container, a label on the container and a composition of comprising a method of treating an immune related disease in a mammal; (10) a method of treating an immune related disease in a sample suspected of having the polypeptide; (11) a method of cidentifying a compound that inhibits or composing an immune related disease or an inflammatory immune response companding an immune related disease or an inflammatory immune response companding an extinct of a gene encoding a PRO polypeptide companding an immune response in a mammal; (12) a method of identifying a compound that inhibits or companding an extinct of a gene encoding a PRO polypeptide companding an extinct of a gene encoding a PRO polypeptide companding an extinct of a gene encoding a PRO polypeptide companding an extinct of a gene encoding a PRO polypeptide companding an extinct of a gene encoding a PRO polypeptide companding an encoded polypeptide, compositions, kits and methods are compositions, kits and methods are consecuted to useful in diagnosing and treating an immune related disease and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 707; 3009pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                erythematosus, rheumatoid arthr stimulating an immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New PRO polynucleotides and polypeptides, useful in useful in diagnosing and treating an immune related disease, e.g. systemic lupus erythematosus, rheumatoid arthritis, diabetes mellitus or asthma and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-OCT-2002; 2002US-0422472P
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                                         useful in diagnosing and treating an immune related disease and in
stimulating an immune response. The present sequence represents a l
PRO protein from the present invention.
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Wood WI, Wu
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Search completed: November 29, 2005, 22:52:14 Job time: 117.545 secs
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                                                                                                                                      Query Match 100.0%; Score 64; DB 3; Best Local Similarity 100.0%; Pred. No. 0.015; Matches 12; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                            The present sequence represents the human ribosome recruitment protein elF4G1. The protein is used for the translational activation of genes. The elF4G1 protein is an RNA-binding protein. The protein is also used for the translation of RNA molecules containing protein binding sites, identifying RNA-binding proteins, protein-protein interactions, or inhibitors or enhancers of the interactions, providing a cell or subject with therapeutic proteins, controlling the levels of translation of the therapeutic proteins, controlling the translation and stockhometry of multiple subunit proteins, screening proteins that interact with an RNA binding site, and identifying the RNA binding sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid encoding an RNA with a coding region and protein binding sites in an adjacent 5' non-coding region for translational activation of genes using the ribosome recruitment protein eIF4G.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 9A-H; 140pp; English.
                                                                                                                                                                                                                Sequence 1560 AA;
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N-PSDB; AAA75835.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-MAR-1999;
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                                                                                            1 KKRYDREFLLGF 12
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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seq length: 2000000000
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Match
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2005 Compugen Ltd.
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AAB31452
AAB1107
AAB1107
ADT60579
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ADQ157031
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AAB11103
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AAG47553
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Aab31447 Peptide d
Aab31452 Peptide d
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Adq37031 Cell prol
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Peptide d
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Arabidops
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A. thalia
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62.7		62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	62	. 62.7	62.7	62.7	64.4		64.4	4	64.4
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Abu47291				-		v			Aar86956		-			•	. œ	_	α			φ
Protein e	Procein e	E. COLL P		E. coll p	ino ac	Photornab	Amino aci	Disease t	E. coll p			۲	റ	Listeria	E. COLL P	C)	Arabidops	Plant acy	Arabidops	Arabidops

# ALIGNMENTS

RESULT 1 AAB31439

AAB31439 standard; peptide; 12 AA.

Binding peptide; cell death; cell

A wheat eukaryotic Initiation Factor 4G (eIF4G) binding peptide

eukaryotic Initiation Factor 4G; eIF4G; eIF4E; apoptosis; anticancer; antitumor.

20-APR-2001 (first entry)

AAB31439;

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The present sequence represents a binding peptide for an eukaryotic Initiation Factor 4G (eIF4G) protein. The specification describes eIF4G and eIF4E binding agents, such as peptides or peptidemimetries. These binding agents are used for the induction of cell death. The binding peptides are used for inducing cell apoptosis. They are used in pharmaceutical compositions for anticancer or antitumor treatment of mammalian cells. Specifically, the peptides result in growth inhibition of, or increased cytotoxicity to tumour cells
                                                                                                                                                   Claim 6; Page 31; 46pp; English.
                                                                                                                                                                           Use of eukaryotic Initiation Factor 4E (elF4E) binding agents e.g. elF4E-binding peptide (elF4E-BP) derivatives as anticancer or antitumor agents for inducing apoptosis in e.g. mammalian tumor cells.
                                                                                                                                                                                                                                                                                                                      21-JUN-1999;
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Sequence 12 AA;
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AAG50817 AAG30623 AAG04583

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Query Match

100.0%;

Score

59;

DB 4

Length 12;

AAG50816 AAG04582

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RESULT 3
AAB31452
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AC AAB3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of eukaryotic Initiation Factor 4E (elF4E) binding agents e.g. binding peptide (elF4E-BP) derivatives as anticancer or antitumor \varepsilon for inducing apoptosis in e.g. mammalian tumor cells.
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                   Peptide derived from wheat
                                                     20-APR-2001
                                                                                      AAB31452;
                                                                                                                    AAB31452 standard; peptide; 14
                                                                                                                                                                                                                                                                                                                                             Sequence 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide derived from wheat eukaryotic Initiation Factor 4G (eIF4G)
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Pred. No. 0.00042;
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02-FEB-2000;
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16-FEB-2001
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   (UYMC-) UNIV MCGILL
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and eIF4E binding agents, such as peptides or peptidemimetics. These binding agents are used for the induction of cell death. The binding peptides are used for inducing cell apoptosis. They are used in pharmaceutical compositions for anticancer or antitumor treatment of mammalian cells. Specifically, the peptides result in growth inhibition of, or increased cytoctoxicity to tumour cells. note: the peptide is biotinylated and linked to penetratin
                                                                                                                                                                                                                                                                                                         Eukaryotic initiation factor; eIF4E; transgenic animal; antidiabetic; knockout mutation; 4E-BP1; glucose metabolism; fat metabolism; anorectic; drug; anti-obesity; anti-fat deposition; anti-metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Use of eukaryotic Initiation Factor 4E (elF4E) binding agents e.g. elF4E-binding peptide (elF4E-BP) derivatives as anticancer or antitumor agents for inducing apoptosis in e.g. mammalian tumor cells.
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                                                                                 07-APR-2000; 2000WO-CA000388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB11102 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a peptide derived from an eukaryotic 
Initiation Factor 4G (eIF4G) protein. The specification describes eI
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99US-0128559P.
2000US-0179743P.
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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel non-human transgenic animal (I) whose compared cells and somatic cells contain a knockout mutation in DNA encoding A 4E-BP1 (a member of eukaryotic initiation factor 4E (eIF-4E)-binding protein 1) shows a phenotype of an altered glucose and/or fat metabolism cells compared to a control animal. The products of the invention have antidiabetic and anorectic activity. The non-human transgenic animals are certified and associated diseases. The transgenic animals are certified useful as models for the investigation of light and glucose metabolism, cells useful for selection and identification of modulators of the certified and/or activity of 4E-BP1 and for screening drugs to isolate therapeutic agents which are useful as anti-obesity, anti-fat deposition cells and conserved demonstrates that an alteration of 4E-BP1 in the cells conserved demonstrates that an alteration of 4E-BP1 in the cells conserved demonstrates that an alteration of 4E-BP1 in the cells conserved demonstrates that an alteration of 4E-BP1 in the cells conserved demonstrates that an alteration of 4E-BP1 in the cells conserved demonstrates that an alteration of 4E-BP1 in the cells conserved demonstrates that an alteration of 4E-BP1 can modulate fat conserved demonstrates that an alteration of 4E-BP1 can modulate fat conserved demonstrates that an alteration of 4E-BP1 can modulate fat conserved demonstrates that an alteration of 4E-BP1 can modulate fat conserved demonstrates that an alteration of 4E-BP1 can modulate fat conserved demonstrates that an alteration of 4E-BP1 can modulate fat conserved demonstrates that an alteration of 4E-BP1 can modulate fat conserved demonstrates that an alteration of 4E-BP1 can modulate fat conserved demonstrates that an alteration of 4E-BP1 can modulate fat conserved demonstrates that an alteration of 4E-BP1 can modulate fat conserved demonstrates that an alteration of 4E-BP1 can modulate fat conserved demonstrates that an alteration of 4E-BP1 can modulate fat conserved demonstrates tha
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Matches 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          4E-binding site; 4E-binding protein; 4E-BP; 4E-BP1; chemoresistance; cap-dependent translation initiation repressor; apoptosis; translation initiation factor; elF4E; Ras; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB84407 standard; peptide; 16 AA
                                                                                                                                                                                                                                                                                                                        07-JUN-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                Triticum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-AUG-2001
Inducing apoptosis in a cell in which the apoptosis pathway is inhibited, useful for treating cancer or highly proliferative cells, comprises
                                                                       WPI; 2001-381379/40
                                                                                                               Sonenberg N,
                                                                                                                                                                                                                                02-DEC-1999;
                                                                                                                                                                                                                                                                         01-DEC-2000; 2000WO-CA001465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4E-binding site of a p82 protein.
                                                                                                                                                            (UYMC-) UNIV MCGILL.
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12; Conservative
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                                                                                                                    Polunavsky
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Pred. No.
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                                                                                                                      Bitterman
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RESULT 6
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Matches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   activates apoptosis in Ras-transformed fibroblasts and eliminates Ras-induced chemoresistance. The effects of 4E-BP1 are strictly dependent on its ability to sequester the translation initiation factor elf4E, thereby preventing its assembly into an active pre-initiation complex. The specification describes a method for inducing apoptosis in a cell in which the apoptosis pathway is inhibited. The method comprises decreasing the amount of elf4F pre-initiation complex by sequestration of elf4E, thus relieving an apoptosis block. The method is useful for modulating pro-apoptotic and anti-apoptotic pathways in cells, especially in Ras-transformed cells. Thus, the method is particularly useful for treating cancer. The elf4E sequestering agent, 4E-BP1 or its elf4E binding portion is useful for treating high proliferative cells
                                                                                                                                                                                                                                                                                                                                                                                                                  plant; transgenic; cold tolerance; growth rate; drought tolerance; disease resistance; galactomannan production; heat tolerance; herbicide tolerance; lignin production; extreme osmotic condition tolerance; pathogens resistance; pest resistance; yield improvement; seed oil yield; seed protein yield.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB84401-15 represent 4E-binding sites. 4E-binding protein 1 (4E-BP1) is a repressor of cap-dependent translation initiation, and selectively
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          decreasing the amount of elF4F pre-initiation complex, relieving
                                                                                      New recombinant DNA constructs useful in the field of biochemistry genetics, and in particular for producing transgenic plants with in biological characteristics.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plant polypeptide,
                                                                                                                                                       WPI; 2004-757369/74.
                                                                                                                                                                                                                                              28-APR-2003;
28-APR-2003;
                                                                                                                                                                                                                                                                                           18-DEC-2003; 2003US-00739930
                                                                                                                                                                                                                                                                                                                           28-OCT-2004.
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                                                                                                                                                                                    Kovalic
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                                                                                                                                                                                                                 (KOVA/) KOVALIC D
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                                                           2; SEQ ID NO 10656; 14pp; English.
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2003US-00425115
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Pred. No. 0.00058;
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                                                                                                           improved
                                                                                                                            and
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The invention relates a recombinant DNA construct comprising a polynucleotide having any of 5544 nucleotide sequences (cDNAs (1-5544) and encoding a polypeptide with any of 5544 amino acid

SEQ sequences

ID NO:

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RESULT 7
ADQ37031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local
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Cooper B;
                                                                                                                      26-DEC-2002;
                                                                                                                                                                                     23-DEC-2003; 2003WO-US041200
                                                                                                                                                                                                                                                      22-JUL-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell proliferation-related polypeptide #93.
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                                                           (SYGN ) SYNGENTA PARTICIPATIONS
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                                                                                                                         2002US-0436565P
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Pred. No. 0.04;
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RESULT 8
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    encoding a cell proliferation-related polypeptide. The nucleic acid molecule and the encoded polypeptide, and methods are useful for modulating cell proliferation, senescence, differentiation, developmen and stress response in plants, and for producing enhanced food crops. present sequence represents a cell proliferation-related polypeptide. present sequence is published separately from the main body of the
The invention comprises the amino acid and coding sequences of rice stress-related proteins. The DNA and protein sequences of the invention are useful for regulating and controlling plant maturation and development, including proliferation, senescence, disease-resistance, or
                                                                                                                     New isolated nucleic acids and proteins, useful for producing transgenic plants having improved properties, e.g. tolerance to pests, herbicides, or biotic or abiotic stresses, improved nutritional value, or increased
                                                                                                                                                                                                                                                                                                                                                                                                                                  rice; stress-related protein; plant maturation; plant development; plant proliferation; plant senescence; plant disease-resistance; plant stress response; transgenic plant; pest tolerance; herbicide tolerance; biotic stress tolerance; abiotic stress tolerance; improved nutritional value; increased yield; increased proliferation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rice stress-related protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-OCT-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid molecule encoding a cell proliferation-related polypeptide, useful for modulating cell proliferation, senescence, differentiation, development, and stress response in plants, and for
                                                                             Claim
                                                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                                                                       26-DEC-2002; 2002US-0436564P.
                                                                                                                                                                                                                                                                                                                   23-DEC-2003; 2003WO-US041098.
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                                                                                                                                                                                                                                                                                                                                                                              WO2004061080-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      producing enhanced food
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                                                                                                                                                                                                                                                          (SYGN ) SYNGENTA PARTICIPATIONS
                                                                                                                                                                                 2004-534374/51.
DB; ADQ15700.
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                                                                                                         proliferation.
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                                                                             SEQ
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                                                                           English.
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RESULT 9
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                        The invention relates to novel abiotic stress responsive polynucleotides and polypeptides. Also disclosed are vectors, expression cassettes, host cells, and plants containing such polynucleotides. Also disclosed are methods for using the polynucleotides and polypeptides to alter the responsiveness of a plant to abiotic stress. The invention is useful in agriculture. The nucleic acid is useful for determining whether a test collant has been exposed to an abiotic stress condition. It is also useful for selecting an agent that alters abiotic stress regulated polynucleotide expression in a plant cell, and to identify a homolog or ortholog to an abiotic stress responsive polynucleotide. The nucleic acid molecule and the polypeptide encoded by it are useful in altering the responsiveness of a plant to an abiotic stress, such as cold stress, salt stress, osmotic stress or any of their combinations. The present sequence is used in the exemplification of the invention
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa
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                                                                                                                                                                                                                                                                         New stress-responsive nucleic acid, useful responsiveness of a plant, e.g. cereal, to stress, salt stress or osmotic stress.
                                                                                                                                                                                                                                                                                                                                                                                                                                      22-JUN-2001; 2001US-0300112P.
24-AUG-2001; 2001US-0314662P.
26-SEP-2001; 2001US-033277P.
21-NOV-2001; 2001US-0332132P.
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                                                                                                                                                                                                                                                 Claim
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T, Provart
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D, Zhu T;
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                                                                                             This invention describes a novel non-human transgenic animal (I) whose Germ cells and somatic cells contain a knockout mutation in DNA encoding A 4E-BP1 (a member of eukaryotic initiation factor 4E (eIF-4E)-binding (C protein 1) shows a phenotype of an altered glucose and/or fat metabolism (C when compared to a control animal. The products of the invention have antidiabetic and anorectic activity. The non-human transgenic animals are (C useful as models for the investigation of lipid and glucose metabolism, (C energy homeostasis and associated diseases The transgenic animals are (C also useful for selection and identification of modulators of the carpression and/or activity of 4E-BP1 and for screening drugs to isolate (therapeutic agents which are useful as anti-obesity, anti-fat deposition (C disorder, anti-diabetes and anti-metabolic diseases associated with fat deposition disorders. The effect of the disruption of 4E-BP1 in the knockout mice demonstrates that an alteration of 4E-BP1 can modulate fat
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Matches 8
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                                                                                                                                                                                                                                                                                                                                                              Non-human transgenic animal useful as model for studying lipid and glucose metabolism, has germ and somatic cells containing knockout mutation in DNA encoding eukaryotic initiation factor 4E-binding protein
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                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana.
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                                                       Sequence 16
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                                                                                   growth, glucose metabolism and weight gain in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RVRYSRDQLLDL 12
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                Similarity
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                                                          AA,
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75.0%;
                76.3%;
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Pred. No.
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Pred.
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                No :
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0.24;
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                              Length 16;
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RESULT 11
AAB84408
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AAG47553
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                                                                                                                                                                                          Matches
                                                                                                                                                                                                     Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4E-binding site; 4E-binding protein; 4E-BP; 4E-BP1; chemoresistance; cap-dependent translation initiation repressor; apoptosis; translation initiation factor; elP4E; Ras; cancer.
               18-OCT-2000
                                          AAG47553;
                                                                   AAG47553 standard;
                                                                                                                                                                                                                                              Sequence 16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      decreasing the amount of apoptosis block.
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               (first
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                                                                 protein;
               entry)
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66.7%;
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Pred. No. 0.24
4; Mismatches
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  28-MAY 1999
01-JUN 1999
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18-JUN-1999
21-JUN-1999
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24-MAY-1999;
25-MAY-1999;
27-MAY-1999;
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14-MAY-1999;
18-MAY-1999;
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04-MAY-1999;
05-MAY-1999;
06-MAY-1999;
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19-APR-1999;
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09-MAR-1999
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RESULT 13
AAG47552
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KW Prote
KW hybri
KW termi
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                    Protein identification; signal transduction pathway; n hybridisation assay; genetic mapping; gene expression termination sequence.
 Arabidopsis thaliana
                                                                  Arabidopsis
                                                                                                               AAG47552;
                                                                                                                                    AAG47552 standard;
                                                                                        18-OCT-2000
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||:|:|:||:|
6 RVKYTREQLLEL 187
                                                                                                                                                                                                                                     h 76.3%;
Similarity 66.7%;
8; Conservative
                                                                thaliana protein fragment SEQ ID NO: 59948.
                                                                                        (first entry)
                                                                                                                                                                                                                                                                                   99US-015130JP

99US-015133BP

99US-0153070P

99US-015375BP

99US-015403PP

99US-015403PP

99US-015545BP

99US-015545BP

99US-015655BP

99US-0156596P

99US-0158032PP

99US-0158032PP

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99US-015933PP

99US-016076PP

99US-016076PP

99US-016076PP

99US-016076PP

99US-0161405PP

99US-0161405PP

99US-0161359PP

99US-0161359PP

99US-0161933PP

99US-0161933PP

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99US-0161933PP

99US-0161933PP

99US-0161993PP

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                                    pathway; metabolic pathway;
expression control; promoter;
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99US-0139899P.
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99US-0140635P.
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99US-014314P.
99US-0144334P.
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99US-0123180 99US-0123180 99US-0123180 99US-0125788 99US-0126764 99US-0126764 99US-0126764 99US-0126714 99US-0130051 99US-0132487 99US-0132487 99US-0132487 99US-0132487 99US-0132487 99US-0132487 99US-0132487 99US-0132487 99US-0132487 99US-0132487 99US-0132487 99US-0132487 99US-0132487 99US-0132487 99US-0132487 99US-0134218 99US-0134219 99US-0134219 99US-0134219 99US-0136722 99US-0136722 99US-0136722 99US-0139451 99US-0139457 99US-0139457 99US-0139457 99US-0139457 99US-0139457 99US-0139457 99US-0139457 99US-0139457 99US-0139457 99US-0139457 99US-0139457 99US-0139457 99US-0139457 99US-0139457 99US-0139457 99US-0139457 99US-0139453 99US-0139453 99US-0139453 99US-0139453 99US-0139453 99US-0139453 99US-0139453 99US-0139453 99US-0139453 99US-0139453 99US-0139453 99US-0139453 99US-0139453 99US-0139453 99US-0139453	2000EP-00301439.	
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RESULT 14
AAG47551
ID AAG477
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XX 18-OC
XX 18-OC
XX Prote
KW Prote
KW hybri
XX termi
XX PROBE
XX PROBE
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29-SEP-1999
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06-OCT-1999
11-OCT-1999
                                                                                                                        Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                             Arabidopsis thaliana protein fragment SEQ ID NO: 59947.
                                                                                                                                                                                                                                    AAG47551;
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               25-FEB-2000; 2000EP-00301439
                                           06-SEP-2000
                                                                    EP1033405-A2
                                                                                                Arabidopsis thaliana
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Similarity 66.7%;
8; Conservative
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RVKYTREQLLEL 194
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99US-0154779P

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99US-0157853P

99US-015823P

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99US-0140354P.
99US-0140354P.
99US-0141284P.
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RESULT 15
ADX66331
ID ADX66
XX ADX66
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                                                                                                                                                                                                                                        plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance, drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield; yield;
06-MAY-1999; 99US-00304517.
05-NOV-2001; 2001US-00985678.
                                                           28-APR-2003; 2003US-00425114.
                                                                                                     19-FEB
                                                                                                                                           US2004034888-A1.
                                                                                                                                                                                   Unidentified
                                                                                                                                                                                                                          protein
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                                                                                                                                                                                                                                                                                                                                                                                                         polypeptide segid 37174.
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Pred. No. 20;
4; Mismatches
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Search completed: November 29, 2005, 22:52:17 Job time : 117.545 secs
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                                                                                                                                                                                                                                                                           The invention describes a recombinant DNA construct comprising a conjunct consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at the sequence encoding an amino acid sequence ftp. seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for mproving plant tolerance to cold, heat, drought, herbicides, extreme commotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring conformation in plant disease, for producing galactomannan, conformation in plants, for improving yield by modification of plant growth regulators, for increasing the rate of homologous crecombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake cor by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This is the amino acid sequence of a plant full length insert complypeptide that can be used in the recombinant DNA construct of the
                                                                                                                                                Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens pests, for conferring increased resistance to plant disease, or for improving yield.
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(ZHOU/)
(KOVA/)
(SCRE/)
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KOVALIC D K.

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### ALIGNMENTS

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translation initiation factor eIF-4F isozyme form subunit p82 - wheat C;Species: Triticum sp. (wheat)
C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul
C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul
C;Accession: A44452
R;Allen, M.L.; Metz, A.M.; Timmer, R.T.; Rhoads, R.E.; Browning, K.S.
J. Biol. Chem. 267, 23232-23236, 1992
A;Title: Isolation and sequence of the cDNAs encoding the subunits of A;Reference number: A44452; MUID:93054655; PMID:1385417
A;Accession: A44452
                             A,Gene: bla
A,Gene: bla
A,Start codon: GTG
A,Start codon: GTG
C,Superfamily: Beta-lactamase I
C,Superfamily: Beta-lactamase I
C,Keywords: antibiotic resistance; hydrolase; penicillin resistance
F,1-29/Domain: signal sequence #status predicted <SIG>
F,30-302/Product: beta-lactamase I #status predicted <MAT>
F,85/Active site: Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                     R;Coque, J.J.R.; Liras, P.; Martin, J.F.
EMBO J. 12, 631-639, 1993
A;Title: Genes for a beta-lactamase, a penicillin-binding protein
A;Reference number: S36188; MUID:93178438; PMID:8440253
A;Accession: S36188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    beta-lactamase (EC 3.5.2.6) I precursor - Streptomyces lactamdurans
C;Species: Streptomyces lactamdurans
C;Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 05-Oct-2004
C;Accession: S36188; S22750
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C;Genetics:
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A;Note: sequence extracted from NCBI backbone (NCBIP:1182)
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T22182
hypothetical protein F44F1.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Cct-1999 #sequence_revision 15-Oct-1999 #text_change
C;Accession: T22182; T23650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                glycosyltransferase UU503 [imported] - Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: F82883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vankken, S.E.; Umayam, L.; Tallon, L. D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, C. Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable RNA-binding protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
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A;Residues: 1-312 <GLA>
A;Cross-references: UNIPARC:UPI00000C1C98;
A;Experimental source: serovar 3; biovar 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Reference number: A82870
A;Accession: F82883
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R;Glass, J.S.; Heiner, C.R.; Chen, submitted to GenBank, February 2000
A;Description: The complete sequence of Ureaplasma urealyticum: i
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                                                                                                RESULT 5
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A;Gene: At2g22090
A;Gene: At2g22090
                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-347 <STO>
A;Cross-references: UNI
                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Reference number: A84420;
A;Accession: H84608
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                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
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Best Loc
Matches
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ic code: SGC3
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                                                                                                                                                                                                                                                                                                                                                                   UNIPROT:Q9SHZ6; UNIPARC:UPI000017A786; GB:AE002093; NID:g4587587;
                                                                                                                                                            78
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77.8%;
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                                                                                                                                                                                                                                 Score 39; DB
Pred. No. 15;
2; Mismatches
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Pred. No. 13;
2; Mismatches
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                                                                                                                                                                                                                                              DB
15;
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                       09-Jul-2004
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C;Accession: B96501

R;Theologis, A.; Ecker, J.R.; Palm, C. Chin, C.W.; Chung, M.K.; Conn, L.; Co ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu,
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A;Gene: BH2264
C;Superfamily: ompR protein; response regulator homology
                                                                                                                                                                                                   A;Residues: 1-231 <STO>
A;Cross-references: UNIPROT:Q9KAM3; UNIPARC:UPI00000C3E63; GB:AP001514; GB:BA000004;
A;Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                 R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirr
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Map position: 1
A;Introns: 98/1; 375/1; 487/1; 657/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, October 1996 A;Reference number: Z19527 A;Accession: T22182
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                                                                                                                                                                                                                                                                                                                                                                                                                             two-component response regulator BH2264 [imported] - Bacillus halodurans (strain C;Species: Bacillus halodurans
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                                                                                                                                                                                                                                                            A; Molecule type: DNA
                                                                                                                                                                                                                                                                           A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                         C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
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                                                                         Matches
                                                                                         Query Match
Best Local
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                                                                     Local Similarity nes 7; Conserv
                                                                                                                                                                  BH2264
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171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               284
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8; Conserv
                                YSRDQLLDL 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RLKESEDQLLDL 295
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YTREQULDL 179
                                                                         Conservative
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                                                                                       64.48;
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66.7%;
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                                                                         Mismatches
                                                                                         Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 39; DB
Pred. No. 39;
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                                                                                   DB . 15;
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                                                                                                          Length 231;
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NID

hypothetical protein F2J6.12 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar\_2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004

C.J.; Federspiel, N.A.; Conway, A.B.; Conway, A

iel, N.A.; Kaul, S.; White, O.; Alonso, Conway, A.R.; Creasy, T.H.; Dewar, K.;

Johnson-Hopson, C.; Khan, S.; S.X.; Liu, Z.A.; Luros, J.S.;

Khaykin, E.; Kim, C. Maiti, R.; Marziali,

B96501 RESULT 7

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probable acyl CoA synthetase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: O2-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: G96530
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alons
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K
Chin, C.W.; Chung, M.K.; Conn, L.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
Nature 4
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A; Gene: F2J6.12
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A; Residues: 1-613 <STO>
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                                                                                                                                                                                                                         C;Species: Brassica napus (rape)
C;Date: 21-May-1999 #sequence_re
C;Accession: T07928
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C, Superfamily:
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A;Residues: 1-665 <STO>
A;Cross-references: UNI
                                                                                                                               submitted to the EMBL Data Library, April A,Reference number: Z16223
                                                                                                                                                                                                                                                                                                                       probable long-chain-fatty-acid-CoA ligase
N,Alternate names: acyl CoA synthetase
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                                                                                             A; Reference number: A; Accession: T07928
                                                                                                                                                                                                 R, Fulda, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
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Best Local
Status: translated from Molecule type: mRNA Residues: 1-666 <FUL>
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                                                                                                                                                                                                                                                            #sequence_revision
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58.3%;
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Pred. No.
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A;Title: Cloning of the gene encoding streptococcin A-FF22, a novel lantibiotic producet A;Reference number: A58598; MUID:93319301; PMID:8328813
A;Accession: T09007
A;Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-689 <HYN>
A,Residues: 1-689 <HYN>
A;Cross-references: UNIPROT:031053; UNIPARC:UPI00000AF8A4; EMBL:AF026542; NID:g2502065; A;Experimental source: strain FF22
C;Genetics:
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C;Keywords: acid-thiol ligase; coenzyme A
F;100-646/Domain: acetate-CoA ligase homology <ACL>
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A;Experimental source: cv. Ascari; 20-26 days after flowering; developing pods
C;Function:
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C;Superf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABC-transporter homolog ScnT - Streptococcus pyogenes
C;Species: Streptococcus pyogenes
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T09007
C;Accession: T09007
R;Hynes, W.L.; Ferretti, J.J.; Tagg, J.R.
Appl. Environ. Microbiol. 59, 1969-1971, 1993
Appl. Environ. Microbiol. 59, 1969-1971, 1993
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A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein CC0846 [imported] - Caulobacter crescentus C;Species: Caulobacter crescentus C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
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                                                                                                                                                     A;Residues: 1-158 <STO>
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                                                                                    A;Gene:
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Query Match
Best Local S
Matches 7
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Best Local (
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Best Local
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6; Conserv
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Pred. No. 47;
3; Mismatches
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Pred. No. 49;
3; Mismatches
                        Score 37;
Pred. No.
      Mismatches
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.; Jones, L.M.; Karst, U. Duchaud, E.; Durand, L.; Dussurget, O.; E. Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J., A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AE1387
A;Status. Proliminative Comparative Genomics of States Species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J. A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AG1762
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hypothetical protein F35G12.10 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #tex
                                                                           RESULT 14
T21803
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A;Residues: 1-236 <GLA>
A;Cross-references: UNIPROT:0927Z2; UNIPARC:UPI00000CC931; GB:AL592022; PIDN:CAC97871.1
A;Experimental source: strain Clip11262
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Science 294,
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R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, R;Glaser, P.; Frangeul, L.; Buchaud, E.; Durand, L.; I Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; I D.; Jones, L.M.; Karst, U.
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A;Molecule type: DNA
A;Residues: 1-236 <GLF
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001
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A;Experimental source: strain EGD-e
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Best Local (
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#sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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Pred. No.
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Pred. No. 23;
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23;
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Voss, H.; Wehland,
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Search completed: November 29, Job time: 20.8182 secs

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submitted to the EMBL Data Library, October 1994
A;Reference number: Z19473
A;Accession: T21803
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-301 <WIL>
                                                                                                                                                                                   C;Genetics:
A;Gene: VC0900
                                                                                                                                                                                                                                                                                                                               A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae A;Reference number: A82035; MUID:20406833; PMID:10952301 A;Accession: D82265
                                                                                                                                                                                                                                                                                                                                                                                         R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P. l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGDEF family protein VC0900 (imported) - Vibrio cholerae (strain N16961 serogroup C;Species: Vibrio cholerae C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004 C;Accession: D82265
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R;Chui, C.
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A;Experimental source: serogroup O1; strain N16961; biotype El Tor
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A; Residues: 1-524 <HEI>
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A; Map position: 3
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   Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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   protein search, using
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1: uniprot_sprot:*
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   2166443 seqs, 705528306 residues
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Copyright (c) 1993 - 2005 Compugen Ltd.
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01-JUN-2003 (TrEMBLrel. 25, Last sequence update)
01-GUN-2003 (TrEMBLrel. 25, Last sanotation update)
01-GCT-2003 (TrEMBLrel. 25, Last annotation update)
Eukaryotic initiation factor-like protein.
07yza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideee; Oryzeae; Oryza.
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1- FUNCTION: Functions in close association with EIF4B
ATP-despendent RNA-unwinding.
-I- MISCELLANEOUS: In higher plants two isoforms of EIF4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=93054655; PubMed=1385417;
Allen M.L., Metz A.M., Timmer R.T., Rhoads R.E., Browning K.S.;
"Isolation and sequence of the CDNAs encoding the subunits of the isozyme form of wheat protein synthesis initiation factor 4F.";
J. Biol. Chem. 267:23232-23236(1992).
  MEDLINE=22584437; PubMed=12684538; DOI=10.1073/pnas.0737574100; Cooper B., Clarke J., Budworth P., Kreps J., Hutchison D., Park S., Guimil S., Dunn M., Luginbuhl P., Ellero C., Goff S.A., Glazebrook J.;
                                                                                                                                                                                                                                                                                                                                                                                                     Q84PB3 ORYSA PRELIMINARY;
Q84PB3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct protein sequencing; IniRNA-binding.
SEQUENCE 788 AA; 86295 MW;
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InterPro; IPR003891; IF eIF4G_MA3.
Pfam; PF02854; MA3; 1.
Pfam; PF02854; MIF4G; 1.
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411-419; 448-458 AND
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HSSP; O43432; 1HU3.
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Triticeae; Triticum.
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                                                                                       NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Belongs to the eIF4G family.
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12; Conserv
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SM00543; MIF4G; 1.
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yta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
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RESULT 4
Q7XT80 OYYSA
ID Q7XT80 O
AC Q7XT80 O
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Best Local
                                                                                                                                                                                                                                                                                                                      MEDLINE=22337377; PubMed=12447439; DOI=10.1038/nature01183; Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J., Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y., Weng Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D., Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J., Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H., Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y., Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang Y., Zhang W. Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W., Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y., Han B.;
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GO; GO:0003723; F:RNA binding; IEA.
GO; GO:0006412; P:protein biosynthesis; IEA.
InterPro; IPR003890; IF eIF4G.
InterPro; IPR003891; IF_eIF4G_MA3.
Pfam; PF02847; MA3; 1.
Pfam; PF02844; MA3; 1.
SMART; SM00544; MA3; 1.
SMART; SM00543; MIF4G; 1.
                                                                                                                                                                                                "Sequence and analysis of rice chromosome Nature 420;316-320(2002).

EMBL; AL606594; CAE01628.3; -; Genomic_DNAGO; GO:0003723; F:RNA binding; IEA.

SEQUENCE 923 AA; 102231 MW; FC90A2B43E
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01-OCT-2003 (TrEMBLrel.
13-SEP-2005 (TrEMBLrel.
13-SEP-2005 (TrEMBLrel.
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EMBL; AY224450;
HSSP; O43432; 1H
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Name=OSJNBa0029H02.9;
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                            1 RVRYSRDQLLDL 12
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Last sequence update)
Last annotation update)
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                                                                                                                           Score 52;
Pred. No.
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Pred. No.
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IEA.
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RESULT 5
Q6K641 ORYSA
ID Q6K641 ORYSA I
AC Q6K641;

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                                                                    HSSP; 043432; iHU3.
GO; GO:0003723; F:RNA binding; IEA.
GO; GO:0003743; F:translation initiation fa
GO; GO:0003743; F:translation initiation fa
GO; GO:0006412; P:protein biosynthesis; IEA
InterPro; IPR003890; IF eIF4G.
InterPro; IPR003891; IF eIF4G_MA3.
Pfam; PF02847; MA3; 1.
Pfam; PF02847; MA3; 1.
SMART; SM05443; MIF4G; 1.
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05-JUL-2004
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Sasaki T., Matsumoto T., Katayose Y.;
Sasaki T., Matsumoto T., Katayose Y.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP005286; BAD19680.1; -; Genomic_DNA.
Gramene; Q6K641; -.
Gramene; Q6K641; -.
GO; GO:0003733; F:translation initiation factor activity.
GO; GO:0006412; P:prottein biosynthesis; IEA.
GO; GO:0006412; P:prottein biosynthesis; IEA.
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(Iso)4F p82-4).
Name=001004 A05.11;
Oryza sativā (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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GO; GO:000373; F:RNA binding; IEA.
GO; GO:0003743; F:rranslation initiation factor activity; IEA.
GO; GO:0003743; P:protein biosynthesis; IEA.
InterPro; IPR003890; IF_eIF4G.
InterPro; IPR003891; IF_eIF4G_MA3.
Pfam; PF02847; MA3; 1.
Pfam; PF02847; MA3; 1.
SMART; SM00543; MIF4G; 1.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last sunotation update)
Eukaryotic initiation factor 4, eIF4-like protein.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                "Structural analysis of Arabidopsis thaliana (
Sequence features of the regions of 1,367,185
physically assigned Pl and TAC clones.";
DNA Res. 5:203-216(1998).
EMBL; AB013396; BAB08857.1; -; Genomic_DNA.
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MEDLINE-98403884; PubMed-9734815;
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Q9FJM7;
Q1-MAR-2001 (TrEMBLrel. 1
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9; Conserv
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780 AA; 85988 MW;
       factor.
751 AA;
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IEA.
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RESULT 8
Q8H179 A
C Q8H179 A
AC Q8H179 T
DT 01-MAR-2
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C Eukaryot
GN Name-At5
OC Eukaryot
OC Eukaryot
OC Eukaryot
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Matches 8
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GO; GO:0003743; F:translation initiation fa
GO; GO:0006412; P:protein biosynthesis; IEA
InterPro; IPR003890; IF eIF4G.
InterPro; IPR003891; IF_EIF4G_MA3.
Pfam; PF02847; MA3; 1.
Pfam; PF02847; MA3; 1.
SMART; SM00543; MIF4G; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
NUCLEOTIDE SEQUENCE.
Nguyen M., Karlin-Neumann G., Southwick A., Tripp M., Mirand Nguyen M., Rarlin-Neumann G., Banh J., Carninci P., Chen H Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H., Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozak Ecker J., Theologis A., Davis R.W.; Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, BT002055, AAN72067.1; -; mRNA.
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Eukaryota; Viridiplantae; Stropphyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core et
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update
Eukaryotic initiation factor 4, eIF4-like protein.
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                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core everosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-MAR-2003 (TYEMBLYEL 23, I
01-FEB-2005 (TYEMBLYEL 29, I
Eukaryotic initiation factor
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QBH179;
                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta;
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SEQUENCE 776 AA;
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     Southwick
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                         NUCLEOTIDE SEQUENCE.
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r 4, eIF4-like protein.
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Pred. No. 19;
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Chen H.,
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EMBL; BT000467; AAN17444.1; -; mRNA.

REMBL; BT000444; AAO30087.1; -; mRNA.

REMBL; BT003424; AAO30087.1; -; mRNA.

RSP; O43432; 1HU3.

GO; GO:0003723; F:RNA binding; IEA.

GO; GO:0003723; F:RNA binding; IEA.

GO; GO:0003723; P:POTCEIN biosyntheeis; IEA.

InterFro; IPR003890; IF eIF4G.

InterFro; IPR003890; IF eIF4G.

InterFro; IPR003891; IF eIF4G.

INTERFRO; IPR003891; IF eIF4G.

SMART; SM00543; MIF4G; 1.

RSMART; SM00543; MIF4G; 1.

INITIALION factor.

INITIALION factor.
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Yamada K., Banh J., Chan M.M., Q
Deng J.M., Goldsmith A.D., Lee &
Tang C., Toriumi M., Wu H.C., Ya
Carninci P., Chen H., Cheuk R.,
Kamiya A., Karlin-Neumann G., Ki
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-PEC-2005 (TrEMBLrel. 29, Last annotation update)
Putative eukaryotic initiation factor eIF4 (Putat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       initiation factor 4).
Name=At5g57870;
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Q93ZT6;
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Davis R.W.;
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A., Shinozaki K., Davis R.W., I
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Wong C., Wu H.C
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RA Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
RA Fricksen J., Farina A., Faro S., Ferreira P., Fischer H.,
RA Frizgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S.,
RA Gnirke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.
RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
RA Hagopian D., Hagos B., Kamal M., Kambes E., Lewis T.,
RA Lindblad to K., Liu X., Lokyitsang Y., Lucien O.,
RA Kells C., Kieu A., Kisner P., Kodira C., Kulbokas E., Labutti K.,
RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
RA Lindblad-toh K., Liu X., Lokyitsang T., Lokyitsang Y., Lucien O.,
RA Manning J., Marabella R., Maru K., Matchews C., Mauceli E.,
RA McCarthy M., Mcdonough S., Mcghee T., Meldrim J., Meneus L.,
RA McSer J., Mulrain L., Munson G., Naylor J., Newes C., Nguyen C.,
RA Mozes J., Mulrain L., Munson G., Naylor J., Newes C., Nguyen C.,
RA Mozes J., Mulrain L., Munson G., Nelsen C., Nizzari M., Norbu C.,
RA Norbu N., O'donnell P., Okoawo O., O'leary S., Omotosho B.,
RA Norbu N., Schupbach R., Rise C., Rodriguez J., Rogers J., Rogov P.,
RA Rutman M., Schupbach R., Seaman C., Settipalli S., Sharpe T.,
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13-SEP-2005 (TrEMBLrel
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Hypothetical protein.
ORFNames=UM04987.1;
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InterPro; IPR003891; IF_eIF4G_MA3.
Pfam; PF02847; MA3; 1.
Pfam; PF02854; MIF4G; 1.
SMART; SM00544; MA3; 1.
SMART; SM00544; MA3; 1.
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Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
Ustilaginomycetidae; Ustilaginales; Ustilaginaceae;
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RESULT 12
Q5Z5Q3 ORYSA PRELIMINARY;
ID Q5Z5Q3;
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GN Name-OSJNBB0077L03.22;
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-i- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (MGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                        "The full-length cDNA sequences of Schistosoma Submitted (NOV-2004) to the EMBL/GenBank/DDBJ d EMBL; AY816143; AAW27875.1; -; mRNA.

InterPro; IPR003890; IF_eIF4G.
Pf4m; PR02854; MIF4G; 1.
SMART; SM00543; MIF4G; 1.
Hypothetical protein.

SEQUENCE 587 AA; 65922 MW; 06F76764B6984D52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
Schistosoma japonicum (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
Schistosomatoidea; Schistosomatidae; Schistosoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q5D811_SCHJA PRELIMINARY;
Q5D811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
SEQUENCE 108 AA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
   Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=6182;
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,, AACP01000184; EAK85760.1; -; Genomic_DNA.
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8; Conser
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                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                           (TrEMBLrel. 28, Created)
(TrEMBLrel. 28, Last sequence update)
(TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11407 MW;
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66.7%;
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Last annotation updat
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Pred. No. 3.5;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                        2
                                                                                                                                                                                                                                                                                                                                                          Score 43;
Pred. No.
                                                                                           eIF-4F
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                                                                                                                                                                                                                                                                                                                                                                                                             06F76764B6984D52 CRC64;
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databases.
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Q5AZQ2_EMENI
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(T) Clone:OSJNBa0077103.";

(T) Clone:OSJNBa00771;

(T) Clone:OSJNBa0071;

                                                                                                                                 RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavkiy L.,
RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., DAArellano K.,
RA Choepel Y., Collymore A., Cook P., FitzGerald M., Gage D., Galagan J.,
RA Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J.,
RA Erickson J., Faro S., Graham L., Grand-Pierre N., Hafez N.,
RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Matthews C., Mauceli E., McCarthy M., Meddrim J., Meneus L.,
RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
RA Mibova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,
RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA Roman J., Schauer S., Schupback R., Seaman S., Severy P., Smirnov S.,
RA Roman J., Schauer S., Schupback R., Seaman S., Severy P., Smirnov S.,
RA Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
Vernan D. Venner G. Zainoun J., Zembek L., Zimmer A., Zody M.,
Warner R., Venner G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Na, Venner A., Zody M.,
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Best Local
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Q5AZQ2;
10-MAY-2005 (TrEMBLrel. 30, C
10-MAY-2005 (TrEMBLrel. 30, L
10-MAY-2005 (TrEMBLrel. 30, L
10-MAY-2005 (TrEMBLrel. 30, L
Hypothetical protein.
QRENamee=AN6228.2;
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Pfam; PF00642; zf-CCCH; 3.
SMART; SM00543; MIF4G; 1.
SMART; SM00356; ZnF_C3H1; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE
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Burotiales; Trichocomaceae; Emericella.
"Genome Sequence of Aspergillus nidulans.";
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=FGSC
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                                                                                   Wu X., Wyman D., Young G., Zainoun Lander E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    237
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711 AA;
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66.7%;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2F05890B59C9DBC2 CRC64;
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                                                                                                                       Wang S., Wi
Zimmer A.,
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RESULT 14
QAVWT9 SUROC
ID QAVWT9;
AC QAVWT9;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Hox9 (Fragment).

GN Name=Hox9;
OS Olkopleura dioica.
OC Eukaryota; Metazoa; Chordata; Urochordata; Appendicular
OC Olkopleuridae; Olkopleura.
OX NCBL_TaxID=34765;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RA Seco H.C., Macland A.D., Edvardsen R.B., Chourrout D.;
RT "Hypervariable and Highly Divergent Intron/Exon Organiz
RT Chordate Olkopleura dioica."
RT Chordate Olkopleura dioica."
RT Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR InterPro; IPR010287; Homeobox.
DR InterPro; IPR012287; Homeobox.
DR InterPro; IPR012287; Homeobox.
DR Pfam; PF00046; Homeobox; 1.
DR PRINTS; PR00021; HOMEOBOX.
DR PRINTS; PR00021; HOMEOBOX.
DR PRINTS; PR00031; HTHREPRESSR.
DR PROSITE; PS00027; HOMEOBOX.
DR PROSITE; PS00027; HOMEOBOX.
DR PROSITE; PS00027; HOMEOBOX.
DR PROSITE; PS00071; HOMEOBOX.
DR PROSITE; PS00071; HOMEOBOX.
DR NON_TER 60
SQ SEQUENCE 60 AA; 7739 MM; 6E183E697E155DF6 CRC64;
RESULT 15

QBY1Y7_RALSO
ID QBY1Y7;
AC QBY1Y7;
AC QBY1Y7;
DT 01-WAR-2002 (TrEMBLrel. 20, CDT 01-MAR-2002 (TrEMBLrel. 20, LDT 01-CCT-2003 (TrEMBLrel. 25, LDT 01
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Best Local S
Matches 9
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00152; ATPASE_ALPHA_BETA; UNKNOWN_1.
PROSITE; PS50829; GYF; 1.
Hypothetical protein; Nuclear protein.
SEQUENCE 1524 AA; 161671 MW; 8BF805D0D0266D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Urochordata; Appendicularia;
Oikopleuridae; Oikopleura.
NCBI_TaxID=34765;
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SMART; SM00444; GYF; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000194; ATPase
InterPro; IPR003169; GYF.
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Local Similarity 80.0%;
es 8; Conservativo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AACD01000106; EAA57642.1; -; Genomic_DNA.
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9; Conserv
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   Last sequence update)
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Pred. No.
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Pred. No. 6.7;
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Search completed: November 29, 2005, 23:01:19 Job time: 118.091 secs
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RHSSP; O9WYNO; IKGS.

RHSSP; O9WYNO; IKGS.

RGO; GO:00001567; F:DNA binding; IEA.

RGO; GO:0000156; F:two-component response regulator activity; IEA.

RGO; GO:000166; F:two-component response regulator activity; IEA.

RGO; GO:000160; P:two-component signal transduction system (p. . .; IEA.

RGO; GO:0000160; P:two-component signal transduction system (p. . .; IEA.

RGO; GO:0000160; P:two-component signal transduction system (p. . .; IEA.

RGO; GO:0000160; P:two-component signal transduction system (p. . .; IEA.

RGO; GO:0001610; P:two-component signal transduction system (p. . .; IEA.

RGO; GO:000160; P:two-component signal transduction system (p. . .; IEA.

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RGO; GO:000160; P:two-component signal transduction system (p. . .; IEA.

RGO
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Best Local
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STRAIN-GMI1000;

STRAIN-GMI1000;

MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;

Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,

Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,

Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N.,

Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,

Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,

Weissenbach J., Boucher C.A.;

Weissenbach J., Boucher C.A.;

"Genome sequence of the plant pathogen Ralstonia solanacearum.";

Nature 415.497-502 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50110; RESPONSE REGULATORY; 1.

Complete proteome; DNA-binding; Sensory transduction; Transcription;

Transcription regulation; Two-component regulatory system.

SEQUENCE 232 AA; 25020 MW; FB102E1671C0AA71 CRC64;
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Ralstonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nacute 153:137704(1002).
-1-SUBCELULAR LOCATION: Cytoplasmic (By similarity).
EMBL; AL646059; CAD14078.1; -; Genomic_DNA.
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Pred. No.
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29;
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OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.5
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59
1 RVRYSRDQLLDL 12
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1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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# SUMMARIES

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Sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence	50463, A	35246, A	6, Appii	6, Appli	6, Appli	2, Appli	Z, Appli	.2, Appli	7112, Ap	II, Appi	II, Appi	3614, AD	631, App	_	aleo, Ap	6229, AD	3678, AD	1000

# ALIGNMENTS

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RESULT 3
US-08-481-435-13
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Patent No. 6027906
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Best Local Similarity 66.7%;
Matches 8; Conservative
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APPLICANT: Balgane
APPLICANT: Town,
                                                                                                                                                                       APPLICATION NUMBER: IN 580
FILING DATE: 01-UU-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 940
FILING DATE: 24-NOV-1994
ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: in
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 819-8783
                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 11 Ork
CITY: New York
New Yor
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: No. 6027906el Polypeptides NUMBER OF SEQUENCES: 42
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CURRENT APPLICATION DATA:
                                                                NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/751,344B FILING DATE: 19-No. 6210960-1996
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mino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Town, Christine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Balganesh, Tanjore S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        White & Case
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (617) 345-9100
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Pred. No. 2.8;
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Best Local Similarity 60.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                    TELEPHONE: (212) 819-871
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS LENGTH: 159 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: FORIGINAL SOURCE: ORGANISM: Esch
                                                                                                                                                                                                                                                                                                                            FILING DATE: 01-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9404072-2
                                 MOLECULE TYPE:
ORIGINAL SOURCE:
ORGANISM: Esc
                                                                                                                                                                                                                                           FILING DATE: 24-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 11
                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: IN 580/MAS/94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Balganesh, Tanjore S
APPLICANT: Town, Christine
TITLE OF INVENTION: No. 6027906
                 IMMEDIATE SOURCE:
                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
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ADDRESSEE: White & Case
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/481,435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: New York
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                                                                                                       STRANDEDNESS
                                                                                                                     TYPE: amino acid
                                                                                       OPOLOGY:
                                                                                                                                       ENGTH:
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PARC 0593
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                                 Escherichia coli
                                                                                   linear
                                                                peptide
                                                                                                                                                                                                           (212) 819-8783
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 truncated soluble PBP 1B
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Pred. No. 20;
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Query Match Best Local

62.7%;

Score 37; DB Pred. No. 75;

<u>ب</u>

Length 532;

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RESULT 6
US-09-38-092-183
; Sequence 183, Application US/09538092
; Patent No. 6753314
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
COMPUTER: PATEN: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 24-NOV-1994
ATTONREY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REGISTRATION NUMBER: 1103326-151
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: IN 580/MAS/94 FILING DATE: 01-JUL-1994 PRIOR APPLICATION DATA: APPLICATION NUMBER: SE 9404072-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: NO. 6027906el Polypeptides NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                ORGANISM: Escherichia coli
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/481,435 FILING DATE: 10-JUL-1995 CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: New York
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                                                                                                                                  3 RYSRDQLLDL 12
                                                                                                                                                                Similarity 60. 6; Conservative
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                                                                                                                                                                                   Score 37; DB Pred. No. 79;
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Best Local Similarity :
Watches 6; Conservat
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SOFTWARE: CuraPatSeqFormatter Version 0.9
SEO ID NO 183
                                                                                                                  COMPUTER: IMP PC COMPARIBLE
COMPUTER: IMP PC COMPARIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,435
FILING DATE: 10-UUI-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IN 580/MAS/94
FILING DATE: 01-UUI-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9404072-2
FILING DATE: 24-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
NAME: Sterner, Richard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/08481435 Patent No. 6027906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR PILING DATE: 2000-02-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Giot, Loic APPLICANT: Mansfield,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 62
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Saccharomyces cerevisiae
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number YDR292C
TELEFAX: (212) 354-81
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Balganesh, Tanja APPLICANT: Town, Christine TITLE OF INVENTION: No. 60
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                            RELECOMMUNICATION INFORMATION:
                                                                               NAME: Sterner, Richard J
REGISTRATION NUMBER: 35,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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                                           TELEPHONE:
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                                           (212) 819-8783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     No. 6027906el Polypeptides
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                                                                                      1103326-151
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US-08-481-435-9
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Patent No. 6027906
                                                                                   Query Match
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                                                         Matches
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APPLICANT: Balgane
APPLICANT: Town,
                                                                                                                                                                                                                                                             TELEFAX: (212) 354-811 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: IN 580
FILING DATE: 01-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 940
FILING DATE: 24-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/481,435
FILING DATE: 10-JUL-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IN 580/MAS/94
                                                                                                                                IMMEDIATE SOURCE:
CLONE: pARC046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10036-2787
COMPUTER READABLE FORM:
                                                                                                                                                                       MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                      TELEPHONE: (212) 819-8783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: No. 6027906el Polypeptides
                                                                                                                                                                                                                                                                                 TELEPHONE: (212)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  y Match 62.7%;
Local Similarity 60.0%;
hes 6; Conservative
                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
                                                                                                                                                           ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1155 Av
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: United States ZIP: 10036-2787
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                                                                                                                                                                                                     OPOLOGY:
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 292
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                                                                                                                                                                                                                                  amino acid
RYSKDRILEL 301
                            RYSRDQLLDL 12
                                                                                                                                                                                                                                                                                                                                                      Sterner, Richard
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                                                                                                                                                                                                                                              836 amino acids
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                                                         Conservative
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                                                                                                                                                           Escherichia coli
                                                                                                                                                                                                     linear
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                                                                     62.7%;
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                                                                     Score 37; DB 2; Length 836; Pred. No. 1.2e+02;
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Pred. No. 1.2e+02;
                                                         Mismatches
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RESULT 10
US-08-481-435-8
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                                             Sequence 8, Application US/08481435
Patent No. 6027906
GENERAL INFORMATION:
APPLICANT: Balganesh, Tanjore S
APPLICANT: Town, Christine
TITLE OF INVENTION: No. 6027906el Polypeptides
NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/08481435 Patent No. 6027906
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                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (212) 819-8783
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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FILING DATE: 01-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 940407:
FILING DATE: 24-NOV-1994
ATTORNEY JAGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKST NUMBER: 1103:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 10-JUL-1555
FILING DATE: 10-JUL-1555
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: IN 580/MAS/94
                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
ORIGINAL SOURCE:
                CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: Town, Christine
TITLE OF INVENTION: No. 6027906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                     Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YPE: amino acid
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                                                                                                                                                                                                                                                  300 RYSKDRILEL 309
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                                                                                                                                                                                                                                                                                                                    Similarity 6; Conserv
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1155 Avenue of the Americas
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Pred. No. 1.3e+02;
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CITY: New York STATE: New York COUNTRY: United S ZIP: 10036-2787

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                 Query Match
Best Local Similarity
6; Conserve
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                                                                                                                                                         Sequence 12429, Application US/09489039A

Patent No. 6610836

GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILLNG DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR OF ERO ID NOS: 14342
SEQ ID NO 12429
LENGTH: 855
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-481-435-8
                                                                                                          ; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Sterner, Richard J.

REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-151
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
TELEPHONE: (212) 354-8113
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 6; Conserv
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APPLICATION NUMBER: IN 580/MAS/94
FILING DATE: 01-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9404072-2
FILING DATE: 24-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,435
FILING DATE: 10-JUL-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Escherichia coli
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TOPOLOGY: 15
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3 RYSRDQLLDL 12
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                                                      62.7%;
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                                  4; Mismatches
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Pred. No. 1.3e+02;
                                                      Score 37; DB 2;
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                    0;
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                                                                         Length 855;
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                                    Gaps
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FILE REPERENCE: 107136.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILLING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 30457
LENGTH: 419
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT ; ORGANISM: Triticum aestivum US-09-452-239-42
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US-09-252-991A-30457
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US-09-452-239-42
                                                                                                RESULT 14
US-09-252-991A-28689
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APPLICANT: Rafalski, Antoni J.

APPLICANT: Fader, Gary M.

APPLICANT: Fader, Gary M.

APPLICANT: Cahoon, Rebecca E.

TITLE OP INVENTION: Plant Caffeoyl-CoA O-Methyltransferase
FILE REFERENCE: B91284 US NA
CURRENT APPLICATION NUMBER: US/09/452,239

CURRENT FILING DATE: 1999-12-01

EARLIER APPLICATION NUMBER: 60/110,594

EARLIER FILING DATE: 1998-December-02

EARLIER FILING DATE: 1998-December-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Microsoft Office 97
SEQ ID NO 42
LENGTH: 259
                 Sequence 28689, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 30457, Application US/09252991A Patent No. 6551795
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Best Local
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APPLICANT: Marc J. TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                    Local Similarity 100.0%; 1 es 7; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        306 RYSKDRILEL 315
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Rubenfield et al. NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
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100.0%; Pred. No.
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Pred. No. 52;
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Sequence 19888, Application US/09252991A

Sequence 19888, Application US/09252991A

Patent No. 6551795

REPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

FILLE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 1988

LENGTH: 935

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-19888
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; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
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US-09-252-991A-28689
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Search completed: November 29, Job time: 28.6364 secs
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Best Local Similarity 88.9%;
Matches 8; Conservative
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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-425-115-294192
US-10-425-115-294197
US-10-424-599-231391
US-09-973-473-14
US-10-424-599-2348
US-10-424-599-269495
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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence			sequence	Sequence	Sequence	sequence	sequence		
8591, Ap	8590, Ap	TABET,	858, App	394/, AD	23568, A	1568, Ap	•	13904, A	56420, A	10039, A	76075, A	75215, A	77/41, A	T, Appii	z, Appii	55450, A	THUUT,

# ALIGNMENTS

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APPLICANT: SONENBERG, Nahum
APPLICANT: TREMBLAY, Michel
APPLICANT: TREMBLAY, Michel
APPLICANT: TSUKIAYAMA-KOHARA, KYOKO
TITLE OF INVENTION: NON-HUMAN TRANSGENIC ANIMAL WHOSE
TITLE OF INVENTION: SOMATIC CELLS CONTAIN A KNOCKOUT
TITLE OF INVENTION: ENCODING 4E-BP1
FILE REPERENCE: 51401200400
CURRENT APPLICATION NUMBER: US/09/973,473
CURRENT FILING DATE: 2001-10-03
Sequence 10656, Application US/10739930
Publication No. US20040211190A1
Publication No. US20040211190A1
GENERAL INFORMATION:
APPLICANT: KOVAlic, David K.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21(53377)B
CURRENT APPLICATION NUMBER: US/10/739,930
CURRENT APPLICATION NUMBER: US/10/739,930
CURRENT FILING DATE: 2003-12-18
NUMBER OF SEQ ID NOS: 11088
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Best Local Similarity
Matches 12; Conserv
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SEQ ID NO 13
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PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 60/128,559
PRIOR FILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: 60/179,743
PRIOR FILING DATE: 2000-02-02
NUMBER OF SEQ ID NOS: 27
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TYPE: PRT
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Pred. No. 0.0012;
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TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 239945
LENGTH: 775
             NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 38015
LENGTH: 148
                                                                                                                                                                                                                           Sequence 38015, Application US/10767701 Publication No. US20040172684A1 GENERAL INFORMATION:
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                                                                 APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
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APPLICANT: Kovalic David K
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NAME/KEY: unsure
LOCATION: (1)..(784)
OTHER INFORMATION: unsure at all Xaa locations
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LOCATION: (1)..(775)
OTHER INFORMATION: unsure at all Xaa locations
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Glycine max FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Clone ID: PAT_MRT3847_58696C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Clone ID: TRIAE-23APR03-C564_1.p
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Local Similarity 100.0%;
hes 12; Conservation
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Pred. No. 0.88;
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement; FILE REFERENCE: 38-21(53221)B; CURRENT APPLICATION NUMBER: US/10/437,963; CURRENT FILLING DATE: 2003-05-14; NUMBER OF SEQ ID NOS: 204966
SEQUENCE: 752
TYPE: PDT
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US-10-767-701-38015
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 223562
LENGTH: 234
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Best Local Similarity 83.3%;
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
                                                                                                                                                                                                                                                              APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
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LOCATION: (1)..(234)
OTHER INFORMATION: unsure at all Xaa locations
TYPE: PRT
ORGANISM: Oryza sativa
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ORGANISM: Zea mays
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Pred. No.
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Pred. No. 0.37;
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; OTHER INFORMATION: Clone ID:
US-10-437-963-148037
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US-10-425-115-294192
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LENGTH: 785
TYPE: PRT
ORGANISM: Zea mays
                                     ) OTHER INFORMATION: Clone ID: PAT_MRT3847_58697C.1.pep
US-10-424-599-239946
                                                                                                                         APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (5322) B
FULE REFERENCE: 38-21 (5322) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 239946
LENGTH: 775
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Publication No. US20040214272A1
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Best Local Similarity 83...
Matches 10; Conservative
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Query Match
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Best Local
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihus
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
FILE REFERENCE: 38-21(53222)B
CURRENT FILLING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
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NAME/KEY: unsure
LOCATION: (1)..(785)
OTHER INFORMATION: unsure at all Xaa locations
                                                                        ORGANISM: Glycine max FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE: OTHER INFORMATION: Clone ID: MRT4577_31387C.1.pep
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83.3%;
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   84.7%;
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Pred. No. 1.3;
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   Score 50;
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   DB 4;
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 Length 775;
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US-09-973-473-14
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US-10-424-599-231391
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                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/973,473
CURRENT FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: PCT/CA00/00388
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 60/128,559
PRIOR APPLICATION NUMBER: 60/128,559
PRIOR APPLICATION NUMBER: 60/179,743
PRIOR FILING DATE: 2000-02-02
NUMBER OF SEQ ID NOS: 27
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                                                                                                                   ; TYPE: PRT ; ORGANISM: Arabidopsis thaliana US-09-973-473-14
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APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 231391
LENGTH: 789
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
FEATURE:
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_50969C.1.pep
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Publication No. US20040031072A1
GENERAL INFORMATION:
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Matches 10; Conservative
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SEQ ID NO 14
LENGTH: 16
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Best Local Similarity
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                                     Query Match
Best Local Similarity
Matches 8; Conserv
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APPLICANT: TREMBLAY, MICHE!
APPLICANT: TREMBLAY, MICHE!
APPLICANT: TSUKIAYAMA-KOHARA, KYOKO
TITLE OF INVENTION: NON-HUMAN TRANSGENIC ANIMAL WHOSE GERM CELLS AND
TITLE OF INVENTION: SOMATIC CELLS CONTAIN A KNOCKOUT MUTATION IN DNA
TITLE OF INVENTION: ENCODING 4E-BP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 514012000400
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1 RVRYSRDQLLDL 12
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                                         Conservative
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75.0%;
                                                          76.3%; Score 45; D 66.7%; Pred. No. 0.
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                                            Mismatches
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; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_70754C.1.pep
US-10-437-963-172637
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US-10-437-963-199348
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey F
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
                                                                                                                                                                                                                APPLICANT: Li, Ping

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)8

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 199348

LENGTH: 719
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Sequence 172637, Application US/10437963
Publication No. US20040123343A1
                                                Pest Local Similarity 66.7%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 199348, Application US/10437963 Publication No. US20040123343A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 172637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K. APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                         ORGANISM: Oryza sativa FEATURE:
                                                                                                                                                                                                              TYPE: PRT
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                     RVRYSRDQLLDL 12
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RVKYTREQLLEL 12
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Barbazuk, Brad
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Barbazuk, Brad
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                                                            2; Mismatches
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                                                                               Score 43; DB Pred. No. 50;
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Pred. No. 26;
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RESULT 15
US-10-424-599-156877
; Sequence 156877, Application US/10424599
; Publication No. US20040031072A1
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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 37174
LENGTH: 3P7
TYPE: PPT
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US-10-424-599-269495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 269495, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K

APPLICANT: Chou Yihua

APPLICANT: Chou Yihua

APPLICANT: Cor Yonywei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(5322)B

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 269495

LENGTH: 177

TUTNE OF SEC INOS: 285684
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US-10-424-599-269495
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 37174, Application US/10425114 Publication No. US20040034888A1 GENERAL INFORMATION:
                                                               Matches
                                                                                              Query Match
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ORGANISM: Glycine
                                                                                                                                            OTHER INFORMATION: Clone ID: 700866653_FLI.pep
                                                                                                                                                             ORGANISM: Glycine max FEATURE:
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363
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                             1 RVRYSRDQLLDL 12
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RLKYSRDELLAL 374
                                                               Conservative
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                                                                              71.2%;
66.7%;
                                                                             Score 42; DB 4; Length 397; Pred. No. 40;
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Pred. No.
                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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GENERAL INFORMATION:
APPLICANT: La Roba Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT FILING DATE: 2003-04-28
UNMBER OF SEQ ID NOMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
UNMBER OF SEQ ID NOS: 285684
SEQ ID NO 156877
FEATURE:
NAME/KEY: Unsure
FEATURE:
NAME/KEY: Unsure
FEATURE:
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_112682C.1.pep
US-10-424-599-156877
Search completed: November 29, 2005, 23:10:27 Job time : 94.5455 secs
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542 RLKYSRDELLAL 553
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Maximum DB
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1: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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12.124 Million cell updates/sec
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     Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993 - 2005 Compugen Ltd
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     US-10-467-962B-93

US-11-0485-517-127

US-11-054-515-13040

US-11-054-515-13040

US-11-054-515-13040

US-10-93-626-1406

US-10-821-234-1154

US-10-131-826A-120

US-10-131-826A-120

US-10-131-826A-120

US-10-131-826A-20

US-10-131-826A-20

US-10-131-826A-20

US-10-131-626-612

US-10-793-626-612

US-10-793-626-112

US-10-828-730-117

US-10-828-730-117

US-11-02-762-64

US-11-034-176-148

US-11-034-176-189

US-11-031-869-11

US-10-821-234-1195

US-11-031-869-11

US-10-821-234-1195

US-11-031-869-11

US-10-93-626-3136

US-11-074-176-204
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Sequence 93, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 1036, Ap
Sequence 1406, Ap
Sequence 1154, Ap
Sequence 1154, Ap
Sequence 1172, Ap
Sequence 148, App
Sequence 20, Appl
Sequence 2180, Ap
Sequence 2192, Ap
Sequence 2192, Ap
Sequence 117, App
Sequence 117, App
Sequence 117, App
Sequence 118, App
Sequence 1195, Ap
Sequence 118, App
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LENGTH: 495 TYPE: PRT ORGANISM: Arabidopsis thaliana

RESULT 1 US-10-467-962B-93 US-10-467-962B-93 US-10-467-962B-93 Sequence 93, Applica Publication No. US20 RESEAL IMPORMATION: APPLICANT: Blau, A APPLICANT: Blau, A APPLICANT: BLAU, A APPLICANT: BLAU, A APPLICANT: COMMENTION: CURRENT APPLICATION CURRENT FILING DATE: PRIOR APPLICATION N PRIOR FILING DATE: NUMBER OF SEQ ID NO SOFTWARE: PATENTIN SEQ ID NO SOFTWARE: PATENT SEQ ID NO SOFTWARE: PATENTIN SEQ ID NO SOFTWARE: PAT		4 4 4 4 4 4 4 0 9 8 8 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
7-962B-93 ILION NO. US20 ILION NO. US20 INFORMATION: ANT: Plesch, ANT: Blau, A ANT: Klain, DAGENTION: EFERENCE: 200 WT APPLICATION WT FILING DATE APPLICATION FILING DATE FILING DATE APPLICATION FILING DATE FILI		28 28 28 28 28 28 28 28 28 28 28 28 28 2
10-467-962B-93 -10-467-962B-93 Sequence 93, Application US/104 Publication No. US20050246784A1 GENERAL INFORMATION: APPLICANT: Placeh, Gunnar APPLICANT: Blau, Astrid APPLICANT: Blau, Astrid APPLICANT: Caeschner, Klaus APPLICANT: Laenchicu TITLE OF INVENTION: Identifica FILE REFERENCE: 2000 857 CURRENT APPLICATION NUMBER: US CURRENT FILING DATE: 2003-08- PRIOR APPLICATION UMBER: PCT/ PRIOR PILING DATE: 2002-02-13 NUMBER OF SEQ ID NOS: 109 SOFTWARE: Patentin Vers. 2.0 SEQ ID NO 93 LENGTH: 495		4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
US/10 0050246784A Gunnar Strid Strid Stridentific 0 857 WMBER: U WMBER: U 1092-02-03 1098-08 1098-09 1098-09		1067 11092 11227 1227 1400 1150 93 93 95 250 250 250 250 250 250 250 250 250 25
ULT 1 10-467-962B-93 10-467-962B-93 equence 93, Application US/10467962B ublication No. US20050246784A1 ENERAL INFORMATION: APPLICANT: Plesch, Gunnar APPLICANT: Dlescher, Klaus APPLICANT: Elau, Astrid APPLICANT: Klein, Mathieu TITLE OF INVENTION: Identification of Herbicidally Active FILE REFERENCE: 2000 857 CURRENT APPLICATION NUMBER: US/10/467,962B CURRENT FILING DATE: 2003-08-14 PRIOR APPLICATION NUMBER: PC7/EP02/01466 PRIOR FULING DATE: 2002-02-13 NUMBER OF SEQ ID NOS: 109 SOPTWARE: Patentin Vers. 2.0 ENGITH 495	ALIGNMENTS	7 US/11/062 7 US/11/062 7 US/11/062 1 US-10-793-626-96 1 US-10-821-234-1045 1 US-10-858-730-71 1 US-10-667-295-52 7 US-11-053-076-80 7 US-11-053-076-80 7 US-11-054-515-1022 1 US-10-793-626-436 7 US-11-093-626-44 1 US-10-821-234-1001 1 US-10-467-9628-41 1 US-10-467-9628-41 1 US-10-793-626-2296 1 US-10-793-626-2296 1 US-10-793-626-2296 1 US-10-793-626-2296 1 US-10-793-626-2296 1 US-10-793-626-2296 1 US-10-131-8268-72 7 US-11-082-389-390
rive Substances		Sequence 3, Appli Sequence 6, Appli Sequence 96, Appl Sequence 1045, Appl Sequence 70, Appl Sequence 71, Appl Sequence 80, Appl Sequence 1022, Ap Sequence 1022, Ap Sequence 436, Appli Sequence 4, Appli Sequence 2010, Ap Sequence 300, Ap Sequence 2306, Ap Sequence 2296, Ap Sequence 2296, Ap Sequence 72, Appl Sequence 72, Appl Sequence 72, Appl Sequence 73, Appl Sequence 390, App Sequence 390, App Sequence 390, App

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Query Match
Best Local Similarity 58.3%; Pred. No. 7.3;
Best Local Similarity 58.3%; Pred. No. 7.3;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps

Qy 1 RVRYSRDOLLDL 12
||:|||:||
Db 422 RVKYYRDYLVQL 433

RESULT 2
US-10-485-517-127
; Sequence 127, Application US/10485517
; Publication No. US20050256299A1
; GENERAL INFORMATION:
APPLICANT: University of Sheffield
APPLICANT: Biosymexus Incorporated
APPLICANT: Mond, James
: TITLE OF INVENTION: Antigenic Polypeptides
: FILE REFERENCE: 191062390
CURRENT APPLICATION NUMBER: US/10/485.517
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: GB 0118825.9
; PRIOR APPLICATION NUMBER: GB 0200349.9
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; PRIOR FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 424
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 127
; LENGTH: 1263
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-485-517-127
                                                                                                                                                                                                                                                                                                                                                                                                                                    US-11-054-515-3040
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Sequence 17, Application US/11061869
Publication No. US20050256074A1
GENERAL INFORMATION:
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US-11-061-869-17
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PRIOR APPLICATION NUMBER: 60/543/296
PRIOR FILING DATE: 2004-02-11
PRIOR PELLORITON NUMBER: 60/580,347
PRIOR FILING DATE: 2004-06-18
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR FILING DATE: 2002-11-14
PRIOR PELICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR APPLICATION NUMBER: 60/293,499
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PRIOR FILING DATE: 1999-11-30
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 17
LEUGTH: 396
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3040, Application US/11054515 Publication No. US20050255532A1
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Best Local s
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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATING LYMPHOCYTE ACTIVITY
FILE REFERENCE: CIBT-P01-080
CURRENT APPLICATION NUMBER: US/11/061,869
CURRENT FILING DATE: 2005-02-18
                                                                                                                                                                                                                                                              APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523P3
CURRENT APPLICATION NUMBER: US/11/054,515
CURRENT FILING DATE: 2005-02-10
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nes 7; Conserv
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Similarity 58.3%;
7; Conservation
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77.8%;
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Pred. No. 21;
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Pred. No.
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; Remaining Prior Application d;
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1636
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1636
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CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR FILING DATE: 2004-01-14
PRIOR FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR APPLICATION NUMBER: 60/340,817
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PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-01-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 3040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1636, Application US/11054515 Publication No. US20050255532A1 GENERAL INFORMATION:
                                                                                     Matches
                                                                                                                               Query Match
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
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PRIOR FILING DATE: 2001-05-25
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PRIOR FILING DATE: 2001-06-1
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108
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YWRDELLD 115
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                                                                                     Conservative
                                                                                                          52.5%;
75.0%;
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75.0%;
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                                                                                     1; Mismatches
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Pred. No.
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Pred. No. 1
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RESULT 6 US-10-793-626-1406 ; Sequence 1406, Application US/10793626

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RESULT 8
US-10-793-626-1712
; Sequence 1712, Application US/10793626
; Sequence 1712, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
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US-10-821-234-1154
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TITLE OF INVENTION: STARHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS /
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 1406
LENGTH: 415
TYPE: TAMES

LENGTH: 415
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Best Local S
Matches 7
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Best Local (
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GENERAL INFORMATION:
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SEQ ID NO 1154
LENGTH: 495
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NAME/KEY: MOD RES
LOCATION: (415)
OTHER INFORMATION: variable amino acid
-10-793-626-1406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
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APPLICANT: Stache-Crain, Birgit
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Pred. No.
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Pred. No.
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C18
CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR APPLICATION NUMBER: 60/056974
PRIOR APPLICATION NUMBER: 60/056974
PRIOR APPLICATION NUMBER: 60/056974
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
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OTHER INFORMATION: Description OTHER INFORMATION: amino acid US-10-793-626-1712
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1712
                                                               PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR PILING DATE: 1997-09-18
PRIOR PILING DATE: 1997-09-19
PRIOR FILING DATE: 1997-09-19
PRIOR FILING DATE: 1997-09-19
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CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
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Local Similarity 50.0%;
es 5; Conservation
                                                                                                                                                                                                                                                                       FILING DATE: 1997-09-17
APPLICATION NUMBER: 60/059117
APPLICATION NUMBER: 60/059588
FILING DATE: 1997-09-19
ning Prior Application data removed -
                                                                                                                                                                                                                                                     FILING DATE: 1997-09-
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Gurney, Austin L.
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5. US20050245730A1
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Pred. No. 44;
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Query Match
Best Local Similarity
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US-10-131-826A-148
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                                                                                                  ; ORGANISM: Homo Sapien
US-10-131-826A-148
                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
                                                                                                                                   Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 550 SEQ ID NO 148 LENGTH: 834 TYPE: PRT
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LENGTH: 775
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Best Local Similarity 55.6%;
Matches 5; Conservative
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                                                                                                                                                                                                                                       PRIOR FILING DATE: 1997-09-19
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FILING DATE: 1997-09-18
APPLICATION NUMBER: 60/059352
FILING DATE: 1997-09-19
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Wood, William
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5. US20050245730A1
                  52.5%;
ilarity 54.5%;
Conservative
                  ; Score 31; DB 1; Pred. No. 71; 3; Mismatches
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Pred. No.
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US-10-131-826A-20
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US-10-131-826A-20
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Matches
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PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data rei
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 20
LENGTH: 867
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APPLICANT: Baker, Kevin P.
                                                                                                                          Query Match
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C128
CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR APPLICATION NUMBER: 60/056974
PRIOR APPLICATION NUMBER: 60/056974
PRIOR APPLICATION NUMBER: 60/056978
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PRIOR APPLICATION NUMBER: 60/056913
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PRIOR APPLICATION NUMBER: 60/059263
PRIOR TILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR FILING DATE: 1997-09-19
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PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
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PRIOR FILING DATE: 1997-09-17
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les 6; Conserv
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                                       4 YSRDQLLDL 12
YSKDYLTDL 195
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Watanabe, Colin K
Wood, William
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                                                                                Conservative
                                                                                                  52.5%;
66.7%;
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                                                                                Score 31; DB Pred. No. 74; 1; Mismatches
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RESULT 12 US-10-793-626-1540 ; Sequence 1540, Application US/10793626

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US-10-793-626-612
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TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REPERENCE: PID1480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION UNMBER: 60/164,258
PRIOR APPLICATION UNMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2328
LENGTH: 145
LENGTH: 145
LENGTH: 145
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PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 1540
LENGTH: 138
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Sequence 612, Application US/10793626

Publication No. US20050255478A1

GENERAL INFORMATION:

APPLICANT: KIMMERLY, WILLIAM JOHN

APPLICANT: KIMMERLY, WILLIAM JOHN

TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS

FILE REFERENCE: PU3480US

CURRENT FILING DATE: 2004-03-04

PRIOR APPLICATION NUMBER: 60/164,258

PRIOR FILING DATE: 1999-11-09
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Best Local
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Best Local S
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TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
CURRENT FILING DATE: 2004-03-04
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Similarity 66.7%;
6; Congervarion
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Pred. No. 16;
1; Mismatches
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Sequence 2192, Application US/10793626

; Publication No. US20050255478A1

; GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
ITITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626

CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTMARE: Patentin Ver. 2.1
SEQ ID NO 2192
LENGTH: 286
TYPE: PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Artificial Sequence; PEATURE: OTHER INFORMATION: Description of Artificial Sequence: synthetic; OTHER INFORMATION: amino acid sequence US-10-793-626-612
                                                                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence: synthetic; OTHER INFORMATION: amino acid sequence US-10-793-626-2192
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US-10-793-626-2192
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Search completed: November 29, Job time: 4.25 secs
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 612
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Local Similarity 41.7%;
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267 RIQYNVDDLQDI 278
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3: geneseqp2000
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Copyright (c) 1993 - 2005 Compugen Ltd.
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## SUMMARIES

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ACCO

## ALIGNMENTS

RESULT 1 ABB96919 Human; tumour; antigen; HLA-A2; cytotoxic T cell; cytostatic; cancer; Human tumour antigen related peptide SEQ ID NO 14. 21-JUN-2002 ABB96919; ABB96919 standard; peptide; 9 AA. 31-JUL-2000; 2000JP-00231814. 30-JUL-2001; 2001WO-JP006526. 07-FEB-2002. WO200210369-A1. Homo sapiens. vaccine. (ITOH/) ITOH K. (first entry)

Tumor antigens inducing and/or activating HLA-A2-restricted tumor-specific cytotoxic T cells, useful in diagnosis of and screening drugs e.g. cancer vaccines for specific treatment of pancreatic cancer.

WPI; 2002-291857/33.

Itoh K;

Claim 1; Page 21; 127pp; Japanese.

The invention relates to a peptide comprising an amino acid sequence selected from 44 fully defined amino acid sequences (ABB96906-ABB969549) and a polypeptide comprising an amino acid sequence selected from the 9 fully defined amino acid sequences (ABB969143-ABB97151). The above comprise a tumour antigen inducing or activating HLA-A2-restricted tumour specific cytotoxic T cells, which recognise HLA-A2 and a tumour antigen peptide and is thus activated. The peptides and polypeptides have cytostatic activity. The tumour antigen is useful in diagnosis of and screening drugs for specific treatment of pancreatic cancer, colon cancer and stomach cancer including in the form of vaccines. The present sequence is that of a tumour antigen peptide, useful to the invention

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specific cytotoxic T cells, useful in diagnosis of and screening drugs
e.g. cancer vaccines for specific treatment of pancreatic cancer.
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             ABR84356 standard; peptide;
                                                                                                                                                                                   Sequence 9 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a method for the detection of antigen specific T-cells in a blood sample involving the use of a plurality of antigenic peptides. The method comprises sampling of peripheral blood monocytes; stimulation of the collected peripheral blood monocytes with antigens without direct use of antigen presenting cells; and detection of T-cells specific to the antigen in the stimulated monocytes. The method is particularly used for the detection of cancer as it can be used in semi-quantitative determination of cancer specific T-cells. It can also be used for cancer vaccine therapy for patients with cervical or prostate cancer. The method can additionally be used to monitor of cellular immunity and cancer immune therapy by detection of specific T-cell frequencies. Sequences ABR84350-ABR84365 represent HLA-A2 (human leukocyte antigen) peptides of human origin used in an example from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A detection method of antigen specific T-cells, comprises the use of plural antigenic peptides, useful in semi-quantitative determination of cancer specific T-cell frequencies and for monitoring cellular immunity.
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                                                          Binding peptide; cell death; cell
                                                                                                         A human eukaryotic Initiation Factor 4E (eIF4E) binding peptide.
                                                                                                                                         20-APR-2001
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                                                          eukaryotic Initiation Factor 4G; eIF4G;
apoptosis; anticancer; antitumor.
 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                              100.0%;
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Pred. No.
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cell death; cell
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/label= Lys,
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anticancer; antitumor.
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                      The present sequence represents a binding peptide for an eukaryotic Initiation Factor 48 (eIF4B) protein. The specification describes eland eIF4B binding agents, such as peptides or peptidemimetics. These binding agents are used for the induction of cell death. The binding peptides are used for inducing cell apoptosis. They are used in pharmaceutical compositions for anticancer or antitumor treatment of mammalian cells. Specifically, the peptides result in growth inhibit
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                                                                                                                                                                                                                                                                                             Use of eukaryotic Initiation Factor 4E (elF4E) binding agents e.g. elF4E-binding peptide (elF4E-BP) derivatives as anticancer or antitumor agents for inducing apoptosis in e.g. mammalian tumor cells.
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cell death; cell
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  or increased cytotoxicity to tumour cells
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apoptosis;
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                                                                                                                  germ cells and somatic cells contain a knockout mutation in DNA encoding a 45-BP1 (a member of eukaryotic initiation factor 45 (eIF-4E)-binding protein 1) shows a phenotype of an altered glucose and/or fat metabolism when compared to a control animal. The products of the invention have antidiabetic and anorectic activity. The non-human transgenic animals are useful as models for the investigation of lipid and glucose metabolism, energy homeostasis and associated diseases. The transgenic animals are also useful for selection and identification of modulators of the expression and/or activity of 4E-BP1 and for screening drugs to isolate therapeutic agents which are useful as anti-obesity, anti-fat deposition disorder, anti-diabetes and anti-metabolic diseases associated with fat deposition disorders. The effect of the disruption of 4E-BP1 can modulate fat tissue growth, glucose metabolism and weight gain in an animal
                                                                                                                                                                                                                                                                                                                                                                                                                      Non-human transgenic animal useful as model for studying lipid and glucose metabolism, has germ and somatic cells containing knockout mutation in DNA encoding eukaryotic initiation factor 4E-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryotic initiation factor; eIF4E; transgenic animal; antidiabetic; knockout mutation; 4E-BP1; glucose metabolism; fat metabolism; anorectic; drug; anti-obesity; anti-fat deposition; anti-metabolic.
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                                                                                             Sequence 16 AA;
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                        AAB11095 standard;
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02-FEB-2000; 2000US-0179743P.
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Eukaryotic initiation factor; eIF4E; transgenic animal; antidiabetic; knockout mutation; 4E-BP1; glucose metabolism; fat metabolism; anorectic;
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                                                  Chicken eIF-4E recognition motif peptide 4E-BP
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This invention describes a novel non-human transgenic animal (I) whose CC germ cells and somatic cells contain a knockout mutation in DNA encoding CC a 4B-BP1 (a member of eukaryotic initiation factor 4E (eIF-4E)-binding CC protein 1) shows a phenotype of an altered glucose and/or fat metabolism CC when compared to a control animal. The products of the invention have CC useful as models for the investigation of lipid and glucose metabolism, CC energy homeostasis and associated diseases. The transgenic animals are CC expression and/or activity of 4B-BP1 and for screening drugs to isolate CC therapeutic agents which are useful as anti-obesity, anti-fat deposition disorders. The effect of the disruption of 4E-BP1 in the CC knockout mice demonstrates that an alteration of 4E-BP1 can modulate fat the constrates that an alteration of 4E-BP1 can modulate fat the constrates that an alteration of 4E-BP1 can modulate fat
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kout mutation in DNA encoding factor 4E (e1F-4E)-binding flucose and/or fat metabolism ucts of the invention have n-human transgenic animals are
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protein 1) shows a phenotype of an altered glucose when compared to a control animal. The products of antidiabetic and anorectic activity. The non-human

for treating

protein

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RESULT 15
AAB84404
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4E-binding site; 4E-binding protein; 4E-BP; 4E-BP1; chemoresistance; cap-dependent translation initiation repressor; apoptosis; translation initiation factor; elF4E; Ras; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 16 AA;
            AAB84401-15 represent 4E-binding sites. 4E-binding protein 1 (4E-BP1) is a repressor of cap-dependent translation initiation, and selectively activates apoptosis in Ras-transformed fibroblasts and eliminates Ras-induced chemoresistance. The effects of 4E-BP1 are strictly dependent on its ability to sequester the translation initiation factor elf4E, thereby preventing its assembly into an active pre-initiation complex. The specification describes a method for inducing apoptosis in a cell in which the apoptosis pathway is inhibited. The method comprises decreasing the amount of elf4F pre-initiation complex by sequestration of elf4E, thus relieving an apoptosis block. The method is useful for modulating pro-apoptotic and anti-apoptosis block. The method is useful for treating cancer. The elf4E sequestering agent, 4E-BP1 or its elf4E binding portion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB84404 standard; peptide; 16
                                                                                                                                                                                                                                                                                                       Inducing apoptosis in a cell in which the apoptosis pathway is inhibited, useful for treating cancer or highly proliferative cells, comprises decreasing the amount of elF4F pre-initiation complex, relieving an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2000; 2000WO-CA001465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4E-binding site of a 4E-binding protein
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                                                                                                                                                                                                                                                     Disclosure; Fig 6; 80pp; English
                                                                                                                                                                                                                                                                                         apoptosis block
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Qy 1 RIYDRKFL 9
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and is derived by analysis of the total score distribution.
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   protein search, using sw model
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1: pir1:*
2: pir2:*
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2005 Compugen Ltd.
 A57396
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Query Match Best Local Simi	RESULT 2  A55258  insulin-stimulated phosphoprotein PHAS C; Species: Rattus norvegicus (Norway r C; Date: 06 Feb-1995 #sequence_revision C; Accession: A55258; A54719 - R; Hu, C.; Pang, S.; Kong, X.; Velleca, Proc. Natl. Acad. Sci. U.S.A. 91, 3730 A; Title: Molecular cloning and tissue A; Accession: A55258 MUID: 94224 A; Accession: A55258 A; MUID: 94224 A; Accession: A55258 A; MUIPROT: 062622; UN A; Cross-references: UNIPROT: 062622; UN A; Cross-references: UNIPROT: 07062622; UN A; Cross-references: UNIPROT: 07062622; UN A; Title: Phosphorylation of PHAS-I by A; Molecula type: protein A; Molecula type: protein A; Molecula type: protein A; Residues: 58-69 < HAY A; Cross-references: UNIPARC: UPI0000179 C; Keywords: phosphoryctein C; Ger (co	Qy 1 RII'       Db 50 RII'	Query Match Best Local Simi: Matches 9;	RESULT 1 A57396 PHAS-I protein - mouse C; Species: Mus musculus (house n C; Date: 23-Feb-1996 #sequence_re C; Accession: A57396 R; Lin, T.A.; Kong, X.; Saltiel, J. Biol. Chem. 270, 18531-18538 A; Title: Control of PHAS-I by it A; Reference number: A57396; MUII A; Reference number: A57396 A; Status: preliminary; not compound as a compoun		30 31 32 33 32 33 33 33 33 33 33 33
97.9%; imilarity 100.0%	in-stimulated phosphoprotein PHAS-I cies: Rattus norvegicus (Norway rate: 06 Feb-1995 #sequence revision 0 pession: A55258; A54719 C.; Pang, S.; Kong, X.; Velleca, M. C.; Pang, S.; Kong, X.; Velleca, M. Natl. Acad. Sci. U.S.A. 91, 3730-3 le: Molecular cloning and tissue dierence number: A55258; MUID:9422481 pession: A55258 mRNA idues: 1-117 < HUNPACI (06262; UNIP pecule type: mRNA idues: 1-117 < HUNPACI (06262; UNIP per	RIIYDRKFL 9          RIIYDRKFL 58	97.9%; larity 100.0%; Conservative	nouse sculus (house mouse) sculus (house mouse) sk #sequence_revision 23 6 X.; Saltiel, A.R.; Bla 0, 18531-18538, 1995 0, FPAS-I by insulin in fF PAS-I by insulin in r: A57396; MUID:95355483 6 AST396; mot compared with nENA ACLIN s: UNIPROT:Q60876; UNIPA		68.1 388 2 68.1 454 2 68.1 454 2 68.1 503 2 68.1 505 2
Score 46; DB 2; Length; Pred. No. 0.038;	n PHAS-I - rat vision 06-Feb-1995 #text_cl vision 06-Feb-1995 #text_cl lleca, M.; Lawrence Jr., J , 3730-3734, 1994 issue distribution of PHAS :94224815; PMID:8170978 :94224815; PMID:8170978 22; UNIPARC:UPI00000E729C; 11994 M.M.; Hu, C.; Lin, T.A.; L 11994 -I by mitogen-activated pr :94365019; PMID:8083223  0001796E7 0001796E7		Score 46; DB 2; Length Pred. No. 0.038; 0; Inde	-Feb-1996 #text ckshear, P.J.; 3T3-L1 adipocyt ; PMID:7629182 conceptual tran	ALIGNMENTS	D72200 D72200 PC4237 T37933 H81366 JC6522 JC6522 JC76522 JC76522 JC76526
117;	_change 09-Jul-2004 J.C. AS-I, an intracellular target for the second se		117; els 0; Gaps 0;	change 09-Jul-2004 Lawrence Jr., J.Ces. Synthesis, degradation, and .slation .slation .p. GB:U28656; NID:g881557; PIDM		ornithine decarbox trans-cinnamate 4-transcription acti leucyl aminopeptid trans-cinnamate 4-trans-cinnamate 4-trans-cin

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R;Pause, A.; Belsham, G.J.; Gingras, A.C.;
Nature 371, 762-767, 1994
                                                                                                                                                                                                                                                                                                                                                                                       4E-BP2 protein - human
C;Species: Homo sapiens (man)
C;Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                  A;Title: Insulin-dependent stimulation of protein synthesis by phosphorylation of a regula; Reference number: S50866; MUID:95021760; PMID:7935836
A;Accession: S50867
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A;Molecule type: DNA
A;Residues: 1-118 <NIS>
A;Cross-references: UNIPARC:UPI00006E50A
A;Cross-references: uniparc:upid0006E50A
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A;Residues: 1-118 <PANIPARC:UPI000006E50A; EMB
A;Cross-references: UNIPROT:Q13541; UNIPARC:UPI000006E50A; EMB
A;Cross-references: UNIPROT:Q13541; UNIPARC:UPI000006E50A; EMB
A;Nish1, N.; Morino, S.; Tomoo, K.; Youtan1, T.; Ishida, T.
J. Blochem. 123, 157-161, 1998
A;Title: Expression of a synthetic gene for initiation factor A;Reference number: JC5899; MUID:98162949; PMID:9504423
A;Accession: JC5899; MUID:98162949; PMID:9504423
A;Accession: JC5899; MUID:98162949; PMID:9504423
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C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S50866; JCS899
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A; Residues: 1-120 < PAU>
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F;65/Binding site: phosphate (Ser) (covalent) #status predicted
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Nature 371, 762-767, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N;Alternate names: 4E-BP1
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 51
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                                                                                                         Length 120,
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A; Status; preliminary
A; Status; preliminary
A; Status; preliminary
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residuee: 1-1680 «RODE»
A; Residuee: 1-1680 «RODE»
A; Cross-references: UNIPROT: P30432; UNIPARC: UPI000016BC03; GB: M94375; NID: g157461; PID: g1
A; Cross-references: UNIPROT: P30432; UNIPARC: UPI000016BC03; GB: M94375; NID: g157461; PID: g1
A; Cross-references: UNIPROT: P30432; UNIPARC: UPI000016BC03; GB: M94375; NID: g157461; PID: g1
                                                                                                                                                                                                                                                                                    furin (EC 3.4.21.75) 2 - fruit fly (Drosophila melanogaster)
(;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A4334
R;Rocession: A4334
R;Rocebroek, A.J.; Creemers, J.W.; Pauli, I.G.; Kurzik-Dumke, U.; Rentrop, M.; Gateff, E.;
J. Biol. Chem. 267, 17208-17215, 1992
A;Title: Cloning and functional expression of Dfurin2, a subtilisin-like proprotein proce
A;Reference number: A43434; MUID:92381036; PMID:1512259
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Best Local Similarity
Watches 6; Conserve
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C;Superfamily: phage T4 DNA-directed DNA polymerase
C;Keywords: DNA binding; DNA replication; nucleotidyltransferase
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A;Residues: 338-898 <LAM>
A;Cross-references: UNIPARC:UPI000016D7A7; GB:M37159; GB:M28192; NID:g215839; PIDN:AAA21;
C;Comment: This enzyme is required for both initiation and maintenance of viral DNA repli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPARC:UP1000005CB21; GB:M10160; GB:J02510; GB:X00769; NID:g2947028, R;Lamm, N.; Wang, Y.; Mathews, C.K.; Rueger, W. Bur. J. Biochem. 172, 553-563, 1988
Bur. J. Biochem. 172, 553-563, 1988
A;Title: Deoxycytidylate hydroxymethylase gene of bacteriophage T4: nucleotide sequence capterence number: JP0071; MUID:88166734; PMID:3350013
A;Accession: JU0097
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A;Title: Primary structure of T4 DNA polymerase.
A;Reference number: A28165; MUID:88227938; PMID:3286635
A;Accession: A28165.
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C;Date: 17-Mar-1987 #sequence revision 30-Jun-1987 #text_change 09-Jul-2004
C;Accession: JS0791; PU0006; A28165; JU0097; A00717
                                                                                                                                                                                                                                                         A; Reference number: A43434;
A; Accession: A43434
                              C;Genetics:
A;Gene: FlyBase:Fur2
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A; Residues: 1-898 <SPI>
A;Cross-references: FlyBase:FBgn0004598
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A;Residues: 1-898 <SP3>
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A;Accession: PU0006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;Species: phage T4
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C;Keywords: hydrolase; serine proteinase; transmembrane protein F;409-652/Domain: subtilisin homology <SBT> F;418,457,638/Active site: Asp, His, Ser #status predicted
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C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change
C;Accession: JQ0531
R;Petri, J.B.; Schmieger, H.
Gene 88, 47-55, 1990
A;Title: Isolation of fragments with pac function for phage P22
A;Reference number: PQ0093; MUID:90255967; PMID:2341038
A;Accession: JQ0531
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C, Species: nhace in 7
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A; Residues: 1-162 <PET>
A; Cross-references: UNIPARC: UPT0000136BE0;
C; Comment: This protein is involved in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein AT4g01300 [imported] - Arabidopsis thaliana (foceses: Arabidopsis thaliana (mouse-ear cress) C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004 C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004 C;Accession: A85017
RESULT 9
B96966
beta-mannanase ManB-like enzyme, contains ChW-repeats [imported] -
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A; Residues: 1-291 < STO>
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Best Local Similarity
Matches 7; Conserv
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75.0%;
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Pred. No. 1.1e
1; Mismatches
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Pred. No.
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Pred. No. 28;
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initiation
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C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: B96966
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacte A, Reference number: A96900; MUID:21359325; PMID:21359325
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T01714
                 C;Accession: B86194
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K., ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Scheet, P.; Maggi, L. submitted to the EMBL Data Library, June 1997 A;Description: The sequence of A. thaliana IG A;Reference number: Z14407 A;Accession: T01714
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                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein (imported) - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
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A;Introns: 78/2; 169/1; 234/3; 301/3; 387/3; 528/1; 974/1
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A; Residues: 1-1028 <SCH>
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A;Status: preliminary
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Pred. No. 1e+02;
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C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004 (C;Accession: A85804 (C;Accession: A85804 (R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genca; Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: D90955
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A;Residues: 1-1251 <STO>
A;Cross-references: UNIPROT:Q9MA34; UNIPARC:UPI00000A4622; GB:AE005172; NID:g6850321;
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A;Residues: 1-107 <5TO>
A;Residues: 1-107 <5TO>
A;Cross-references: UNIPROT:Q8XCD6; UNIPARC:UPI00000D04B0; GB:AE005174; NID:g12515970;
A;Experimental source: strain O157:H7, substrain EDL933
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C;Superfamily: Escherichia coli hypothetical protein b1904
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A; Residues: 1-107 < HAY>
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A;Experimental source: strain O157:H7, substrain RIMD 0509952
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/Species: Escherichia coli
/pate: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
                                                                                                                                                                  Superfamily:
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  RLVYDQAFL 43
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Kasunaga, T.; Kuhara, S.;
                                                                                 Conservative
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55.6%;
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Pred. No. 1.3e+02;
3; Mismatches 0;
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K.; Apodaca,
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C;Genetics:
A;Gene: ylbA
C;Superfamily
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C; Bron, S; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho', Bron, S; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho', Bron, S; Bruillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho', A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

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A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler, iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F., Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A; Mathors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y.; Mathors: Lauber, J.; Codega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetellé, R.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetellé, R.; A; Schocher, B.; Rose, M.; Sadaie, Y.; Sato, T.; Sanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot, akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamanoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K. A; Muthors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A, Reference number: A69580; MUID:98044033; PMID:9384377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:P76308;
A;Experimental source: strain K-12,
C;Superfamily: Escherichia coli hypo
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A;Title: The complete genome sequence of Escherichia coli K-12. A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: H64953
                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:034743; A;Experimental source: strain 168
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A; Residues: 1-107 <BLAT>
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C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
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and is derived by analysis of the total score distribution.
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06FF88 BRARE
QTVJN8 HELHP
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RESULT 2

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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Ugdin T.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Romastein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Romastein M.J., Wallano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Rohas S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Shevon M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J.M., Marra M.A.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
                                HGNC; HGNC:3290; 1
MIM; 603483; -.
GO; GO:0016281; C
GO; GO:0030371; F
GO; GO:0045947; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98256334; PubMed=9593750; DOI=10.1074/jbc.273. Poulin F., Gingras A.-C., Olsen H., Chevaller S., Sone "4E-BP3, a new member of the eukaryotic initiation fac protein family.";

Biol. Chem. 273:14002-14007(1998).
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                                                                                                                                                                                                                                                                           uge
                                                                                                                                                                                                                                                                                            This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4EBP3 HUMAN
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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LEU-45, AND TISSUE SPECIFICITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 mouse cDNA sequences.";

C. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)

FUNCTION: Regulates eIF4E activity by preventi

the eIF4F complex.

SUBUNIT: EIF4EBP3 interacts with EIF4E.

TISSUB SPECIFICITY: Expression is highest in s
              GO:0016281; C:eukaryotic translation initiation GO:0030371; F:translation repressor activity; NA GO:0045947; P:negative regulation of translation erPro; IPR008606; EIF4EBP.
                                                                                                                                                                                                                                                                           ae
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SIMILARITY: Belongs to the eIF4E-binding
                                                                                                                                J; AF038869; AAC39761.1; -; n

J; BC010881; AAH10881.1; -; n

J; BC063293; AAH69293.1; -; n

J; BC073751; AAH73751.1; -; n

mbl; ENSG00000131503; Homo (
                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE SPECIFICITY: Expression is highest i heart, kidney, and pancreas, whereas there expression in brain and thymus.
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A Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
A Nicaud S., Jaffe D., Fisher S., Luffalla G., Dossat C., Segurens B.,
A Anthouard V., Jubin C., Castelli V., Boulet N., Castellano S.,
Biemont C., Skalli Z., Cattolicc L., Poulain J., De Berardinis V.,
A Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
A Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
A Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
A Kellis M., Schachter V., Quetier F., Saurin W., Scarpelli C.,
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"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype.";
Nature 431:946-957(2004).
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13-SEP-2005
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Genoscope; Whitehead Institute Centre for Genome Research; Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tetraodon nigroviridis (Green puffer).
Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome 1 SCAF14998, whole genome shotgun sequence.
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Phosphorylation; Protein synthesis
MUTAGEN 40 40 Y->A:
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A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Bilatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stepleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Stepleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glubs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

A Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Bakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Bakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Bakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus
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13-SEP-2005 (Rel. 48, I
Eukaryotic translation
(eIF4E-binding protein
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EMBL; BC061242; AAH61242.1; -; mRNA.
Ensembl; ENSMUSG0000033775; Mus musculus
MGI; MGI:1270847; E1f4ebp3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mouse cDNA sequences.";

(c. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

(c. Natl. Acad. Sci. U.S.A. 99:1
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SIMILARITY: Belongs to the eIF4E-binding protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Swiss-Prot entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on in
37
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                                                                                        μ
                                                                                                                                                                                Similarity 9; Conserv
                                                                                            RIIYDRKFL 9
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                                                                                                                                                                                                                                                                                                                                                                     Protein synthesis inhibitor; Ti
1; 11019 MW; 78F82052696A9BD7
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Last annotation update)
n initiation factor 4E-binding protein 3 (4E-BP3)
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                                                                                                                                                                                                                                 Score 46; DB 1;
Pred. No. 0.17;
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RESULT 5 Q9BG57\_PIG

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RESULT 6
QSUJD2 BRARE
QSUJD2 BRARE PRELIMINARY;
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QSUJD2;
AC
QSUJD2;
DT
O1-FEB-2005 (TrEMBLrel. 29,
DT
O1-FEB-2005 (TrEMBLrel. 29,
DT
O1-FEB-2005 (TrEMBLrel. 29,
DT
O1-FEB-2005 (TrEMBLrel. 29,
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O1-FEB-2005 (TrEMBLrel. 29,
DT
O2c:103720;
GN
ORFNames=2gc:103720;
GN
ORFNames=2gc:103720;
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ORFNames=2gc:103720;
GN
ORFNames=2gc:103720;
GN
CACtinopterygii; Neopterygii;
OC
Actinopterygii; Neopterygii;
OC
Actinoptery R.L., Feingold B.
RA
Klausner R.D., Collins F.S.
RA
Altschul S.F., Zeeberg B.,
RA
Klausner R.D., Collins F.S.
RA
Altschul S.F., Jordan H., Mo
Diatchenko L., Marusina K.,
RA
Altschul S.F., Jordan H., Mo
RA
Diatchenko L., Marusina K.,
RA
Brownstein M.J., Usdin T.B.
RA
Brownstein M.J., Usdin T.B.
RA
Brownstein M.J., Usdin T.B.
RA
Brownstein M.J., Worley K.C., H
RA
Altschul S.F., Morley K.C., H
RA
Altschul S., Worley K.C., H
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Altschul S., Morley K.C., H
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Altschul S., Worley K.C., H
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Altschul S., Kettem
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Bosak S.A., McEwan P.J., Mc
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Brownstein M., Schein J.E., J
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                         RX MEDILINE-2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carriinci P., Prange C.,
RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carrinci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J.M., Warra M.A.,
RA Rodriguez A.C., Grimwood J., Schmutz J.M., Marra M.A.,
RGeneration and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
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Best Local S
Matches 9
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Q9BG57;
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01-JUN-2001
01-MAR-2004
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NON TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; F
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla;
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Pfam; PF05456; eIF_4EBP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sus scrofa (Pig).
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Translation initiation factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brachydanio rerio (zebrafish)
Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; T
Cyprinidae; Danio.
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102 AA;
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5 (TrEMBLrel. 29,
5 (TrEMBLrel. 29,
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) (Danio rerio).
; Craniata; Vertebrata; Euteleostomi;
Teleostei; Ostariophysi; Cypriniformes;
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Pred. No. 0.17;
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                 99:16899-16903 (2002)
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Q98TT6;
10-MAY-2005
submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO85595; AAH85595; 1; mRNA.
ZEIN; ZDB-GENE-041114-44; zgc:103720.
GO; GO:0008190; F:eukaryotic initiation factor 4E binding; IEA.
GO; GO:0045947; P:negative regulation of translational initia.
                                                                                                                                                                                                                                         10-MAY-2005 (Rel. 47, Created)
10-MAY-2005 (Rel. 47, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Eukaryotic translation initiation factor 4E-lA-binding
DEVALUATION (4E-BP).
                                                        ZFIN; ZDB-GENE-030131-3211; zgc:56330.
GO; GO:0005515; F:protein binding; IDA.
GO; GO:0030371; F:translation repressor activity; ISS.
GO; GO:0045947; P:negative regulation of translational initia.
InterPro; IPR008606; EIF4EBP.
                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE [MRNA], AND INTERACTION PubMed=14701818; DOI=10.1074/jbc.M313688200; Robalino J., Joshi B., Pahrenkrug S.C., Jagu "Two zebrafish elf4E family members are difffunctionally divergent."; J., Biol. Chem. 279:10532-10541(2004).
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                                                                                                                  EMBL; AF332983; AAG50053.1; -; mRNA.
EMBL; BC046079; AAH46079.1; -; mRNA.
Ensembl; ENSDARG00000023315; Danio r;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                      This
                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORFNames=zgc:56330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Director MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
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8
                                                                                                                                                                                              European
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NCE 104 AA; 11427 MW;
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9; Conserv
                                                                                                                                                                                                         the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RIIYDRKFL 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR008606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                              rot entry is copyright. It is produced through a collaboration Swiss Institute of Bioinformatics and the EMBL outstation - Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                  its content is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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100.0%; Pred. No.
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                                                                                                                                                                                 nstitute. There are no restrictions of in no way modified and this statement
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differentially expressed
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           CRC64;
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i; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
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RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,

RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,

RA Micaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,

RA Anthouard V., Jubin C., Castelli V., Katlika M., Vacherie B.,

RA Anthouard V., Jubin C., Castelli V., Katlika M., Vacherie B.,

RA Anthouard V., Jubin C., Catelli V., Fullain J., De Berardinis V.,

RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,

RA Cruaud C., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,

RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,

RA Rellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

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RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

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RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

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RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

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RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA Lin
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Best Local S
Matches 9
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Matches
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25-OCT-2004 (TrEMB:
25-OCT-2004 (TrEMB:
25-OCT-2004 (TrEMB:
MGC83416 protein.
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NON TER
SEQUENCE
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Eukaryota; Metazoa; Chordata; Craniata; Verte
Actinopterygii; Neopterygii; Teleostei; Eutel
Acanthomorpha; Acanthopterygii; Percomorpha;
Tetradontoidea; Tetraodontidae; Tetraodon.
   Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Ve;
Amphibia; Batrachia; Anura; Mesobatrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genoscope; Whitehead Institute Centre for Genome Research; Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome 17 SCAF14563, whole genome shotgun seque
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Q4SL38;
                                                                                                                     Name=MGC83416;
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112 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12465 MW;
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Last sequence that the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of th
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Pred. No.
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Euteleostei; Neoteleostei;
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       Pipoidea;
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                                           Euteleostomi;
       Pipidae;
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
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RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RT "Generation and initial analysis of more than 15,000 full-length human
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Best Local S
Matches
                                                                                                  Name=MGC78987;
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Klein S., Gerhard D.S.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, BC075198; AAH75198.1; -; mRNA.
GO; GO:0008190; F.eukaryotic initiation factor 4E binding; IEA.
GO; GO:0045947; P:negative regulation of translational initia.
InterPro; IPR008606; EIF4EBP.
Pfam; PF05456; eIF 4EBP; 1.
SEQUENCE 113 AA; 12459 MW; DAAB4CF04367F1CC CRC64;
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Klein S.L., Strausberg R.L., Wagner
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            TISSUE-Embryo
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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RA Rahing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
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Submitted (Apr-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC068624; AAH68624-1; -; mRNA.
GO; GO:0008190; F:eukaryotic initiation factor 4E binding; IEA
GO; GO:0045947; P:negative regulation of translational initia.
InterPro; IPR008606; EIF4EBP.
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  MEDLINE-2238257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
                                                                                                                                                                                                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Eukaryotic translation initiation factor 4E binding
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                                                                                                                                                                                                                                                    Brachydanio rerio (Zebrafish)
Eukaryota; Metazoa; Chordata;
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                                                                                                                   TISSUE=Kidney;
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                                                                                                                                          NUCLEOTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mouse cDNA sequences.";
c. Natl. Acad. Sci. U.S
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VCE 113 AA; 12430 MW;
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                                                                                                                                          SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=12454917; DOI=10.1002/dvdy.10174; sberg R.L., Wagner L., Pontius J., Clifton S.W.,
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                                                                                                                                                                                                                               h) (Danio rerio).
a; Craniata; Verte
; Teleostei; Ostar
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RA KLausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., RA Altschul S.F., Zeeberg B., Buttown K.H., Schnefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buttown K.H., Schnefer C.F., Bhat N.K., RA Altschul S.F., Zeeberg B., Buttown K.H., Schnefer C.F., Bhat N.K., RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Stapleton M.J., Usdin T.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Roberts M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bonak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Wa Hiting M., Madan A., Touchman J.W., Green E.D., Dickson M.C., A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
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Stapleton M., Soares M.B., Bonaldo M.F., Casvant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
VIllalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
VA Hahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Whiting M., Madan A., Wong A.C., Shevchenko Y., Bouffard G.G.,
Whiting M., Wadan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Whiting M., Wallan W., Green E.D., Dickson M.C.,
Wallakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Whiting M., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.",
In Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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EMBL; BC066546; AAH66546.1; -; mRNA.
ZFIN; ZDB-GENE-031118-83; eif4ebp2.
GO; GO:0008190; F:eukaryotic initiation factor 4E binding; IEA.
GO; GO:0003743; F:translation initiation factor activity; IEA.
GO; GO:0003743; F:negative regulation of translational initia.
InterPro; IPR008606; EIF4EBP.
Pfam; PF05456; eIF 4EBP; 1.
Initiation factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22388257;
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Xenopodinae; Xenopus; Silura
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 AA; 12441 MW;
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(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=12477932; DOI=10.1073/pnas.242603899;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clawed frog) (Silurana tropicalis).
a; Craniata; Vertebrata; Euteleostomi;
Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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Pred. No.
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RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kyosawa H.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Nagili K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanagin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Blake J.A., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Gasterland T., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Kanai A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Maglott D.R., Maltais L., Warchionni L., McKenzie L., Miki H.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
Schoneider C., Semple C.A., Setou M., Shimada K.,
Siltena P. T., Schoneider C., Semple C.A., Setou M., Shimada K.,
Siltena P. T., Schoneider C., Semple C.A., Setou M., Shimada K.,
Schoneider C., Semple C.A., Setou M., Shimada K.,
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE [MRNA], FUNCTION, TISSUE SPECIFICITY, PHOSPHORYLATION, AND INTERACTION WITH EIFAE.
MEDLINE=9535548], PubMed=7629182, DOI=10.1074/jbc.270.31.18531;
Lin T.-A., Kong X., Saltiel A.R., Blackshear P.J., Lawrence J.C.
"Control of PHAS-I by insulin in 373-L1 adipocytes. Synthesis, degradation, and phosphorylation by a rapamycin-sensitive and mit activated protein kinase-independent pathway.";
J. Biol. Chem. 270:18531-18538(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q60876; Q9CZ40;
10-OCT-2003 (Rel. 42, Created)
13-SEP-2005 (Rel. 48, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Eukaryotic translation initiation factor 4E-binding
(eIF4E-binding protein 1) (Phosphorylated heat- and
protein regulated by insulin 1) (PHAS-I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Klein S., Gerhard D.S.; submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases. Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases. EMBL, BC064150; AAH64150.1; -; mRNA. GO; GC:0008190; F:eukaryotic initiation factor 4E binding; IEA. GO; GC:0045947; P:negative regulation of translational initia.
                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
STRAIN=C57BL/6J; TISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodent
Muroidea; Murilae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein. SEQUENCE 113 AA; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
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Schneider C., Sempre Schneider Y., Taylor M.S.,
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA RA Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA RA Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA RA Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
T. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C. Wilming L.G., Wynshaw-Boris A., Yangisawa M., Yang I., Yang L., Yunan Z., Zavolan M., Zhu Y., Zimmer A., Carninci p., Hayatsu N., Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.;
Birney E., Hayashizaki Y.;
Birney E., Hayashizaki Y.;
Birney E., Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between
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                                                                                                                   Ensembl; ENSMUSGO0000031490; Mus musculus.
MGI; MGI:103267; Eif4ebpl.
MGO; GO:0005515; F:protein binding; IPI.
GO; GO:0030371; F:translation repressor activity; TAS.
GO; GO:0030371; F:insulin receptor signaling pathway; IDA.
GO; GO:0006466; F:regulation of translational initiation;
GO; GO:0006466; EIF4EBP.
INTERPROSSOG; EIF4EBP.
                                                                                                                                                                                                                                                                                                               EMBL; U28656; AAA88818.1; -; mRNA.
EMBL; AK013033; BAB28612.1; -; mRNA.
EMBL; BC002045; AAH02045.1; -; mRNA.
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PANTHER; PTHR12669; EIF4EBP; 1.
Pfam; PF05456; eIF 4EBP; 1.
Acetylation; Phosphorylation; Protein synthesis
Translation regulation.
By similarity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mouse cDNA sequences.";

c. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

rUNCTION: Regulates eIF4E activity by preventing its assembly into the eIF4F complex. Mediates the regulation of protein translation by hormones, growth factors and other stimuli that signal through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to insulin, EGF and PDGF.
SIMILARITY: Belongs to the eIF4E-binding protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the MAP Kinase pathway.

SUBUNIT: Nonphosphorylated EIF4EBP1 competes with EIF4G1/EIF4G3 to subunit: Nonphosphorylated EIF4EBP1 caused MAP-kinase (MAPK1 and Interact with EIF4E; insulin stimulated MAP-kinase (MAPK1 and MAPK3) phosphorylation of EIF4EBP1 causes dissociation of the complex allowing EIF4G1/EIF4G3 to bind and consequent initiation of translation. Rapamycin can attenuate insulin stimulation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTM: Phosphorylated on s
to insulin, EGF and PDGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE SPECIFICITY: Highest expression in fat cells. PTM: Phosphorylated on serine and threonine residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mediated by FKBPs
                                                                                                                                                                                                                                                                                                                                                                                                                                        Swiss-Prot entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restrance as long as its content is in no way modified and this s
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7; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                    EIF4EBP.
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Sonenberg N., Lawrence J.C. Jr.;

Sonenberg N., Lawrence mitogen-activated protein kinase and translation initiation.";

Science 266:653-656(1994).

-!- FUNCTION: Regulates eIF4E activity by preventing its assembly into the eIF4F complex. Mediates the regulation of protein translation by hormones, growth factors and other stimuli that signal through the MAP kinase pathway.

-!- SUBUNIT: Nonphosphorylated EIF4EBP1 competes with EIF4G1/EIFG3 to interact with EIF4E, insulin stimulated MAP-kinase (MAPK1 and MAPK3) phosphorylation of EIF4EBP1 causes dissociation of the complex allowing EIF4G to bind and consequent initiation, mediated complex allowing EIF4G to bind and consequent initiation, mediated
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10-QCT-2003 (Rel. 42, Created)
13-SEP-2005 (Rel. 48, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
13-SEP-2005 (Rel. 48, Last annotation update)
13-SEP-2005 (Rel. 48, Last annotation factor 4E-binding
(eIF4E-binding protein 1) (Phosphorylated heat- and
protein regulated by insulin 1) (PHAS-I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AND 97-116, PHOSPHORYLATION, AND TISSUE SPECIFICITY.
STRAIN-Sprague-Dawley; TISSUE-Adipocyte, and Skeletal muscle;
MEDLINE=94224815; PubMed=8170978;
Hu C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry Western C., Pang S. Verry West
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                                                                                                                                                                                                                                                                            -i- TISSUE SPECIFICITY: Expressed in all tissues examined; highest levels in fat and skeletal tissue, lowest levels in kidney.
-i- pTM: Phosphorylated on serine and threonine residues in respons to insulin, EGF and PDGP.
-i- SIMILARITY: Belongs to the eIF4E-binding protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Euarchontoglires; Glires; Roden
Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
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   EMBL; U05014; AAA86938.1; PIR; A55258; A55258.
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                                                                                              removed
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                                                                                                                                                                                   Swiss-Prot entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
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KAlnine N., Chen X., Rolfs A., Halleck A.,
Kalnine N., Chen X., Roffs A., Halleck A.,
Kalnine N., Chen X., Roffs A., Halleck A.,
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10-OCT-2003 (Rel. 42, Created)
13-SEP-2005 (Rel. 48, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
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NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] Ebert L., Schick M., Neubert P., Schat "Cloning of human full open reading fr
                                                                                                                                                                                                                                                                                                                                                      Eukaryotic translation initiation factor 4E-binding (eIF4E-binding protein 1) (Phosphorylated heat- and protein regulated by insulin 1) (PHAS-I).
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                                                     "Cloning of human
                                                                                                                      pancreatic cancer cells.
Submitted (JUN-2000) to
                                                                                                                                                                        NUCLEOTIDE SEQUENCE [MRNA].
                                                                                                                                                                                        MEDLINE=95021760; PubMed=7935836; DOI=10.1038/371762a0; Pause A., Belsham G.J., Gingras A.-C., Donze O., Lin T.-A., Lawrence J.C. Jr., Sonenberg N.; "Insulin-dependent stimulation of protein synthesis by phosphorylation of a regulator of 5'-cap function."; Nature 371:762-767(1994).
                                                                                                                                                                                                                                                       TISSUE=Placenta;
                                                                                                                                                                                                                                                                PHOSPHORYLATION.
                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE [MRNA], FUNCTION, INTERACTION
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                                                                                                                                         "Identification of multiple
                                                                                                                                                             Ito M.,
                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                    sapiens (Human).
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9 RIIYDRKFL 57
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05456; eIF 4EBP; 1.
ion; Direct protein sequencing; Phosphorylation;
synthesis inhibitor; Translation regulation.
                                                                                                                                                                                                                                                                                                                Eutheria;
                                         (MAY-2003)
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                                                                                                                                                                                                                                                                                                                          Metazoa;
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                                                          full-length
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Euarchontoglires; Primates; Cat;
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Phosphoserine (by MA
S->A: Decreases phos
and MAPK3.
R -> N (in Ref. 1; A
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P -> L (in Ref. 1; A
P -> L (in Ref. 1; A
 reading frames
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                                                                                                                                         genes and
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Pred.
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0.19;
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                                                            Creator (TM)
  R.,
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ey T.,
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(by MAPK1 and MAPK3)
phosphorylation by
  Henze S., K
Gateway(TM)
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CRC64;
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acid-stable
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laer J., Lin
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S50866;

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MEDLINE=96091142; PubMed=8521827;
Haghighat A., Mader S., Pause A., Sonenberg N.;
"Repression of cap-dependent translation by 4E-binding
competition with p220 for binding to eukaryotic initial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vector (pDONR201).";
Submitted (JUN-2004)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Exploring proteomes and analyzing protein processing by mass spectrometric identification of sorted N-terminal peptides.";
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                                                                                                                                                                                                                            This Swiss-Prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nat. Biotechnol. 21:566-569(2003).
[7]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Platelet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN SEQUENCE OF 1-12, AND ACETYLATION
                                                                                                                                                                                                                                                             mediated by FKBPs.

INTERACTION:

P06730:EIF4E; NbExp=2; IntAct=EBI-74090, EE
P06730:EIF4EL3; NbExp=1; IntAct=EBI-74090,

PTW: Phosphorylated on serine and threonine
to insulin, EGF and PDGF
to insulin, EGF and PDGF
SIMILARITY: Belongs to the eIF4E-binding px
                                                                                                                                                                    as
                                                                                                                                                                                                                                                                                                                                                                                                                                               OJ. 14:5701-5709(1995).
FUNCTION: Regulates elf4E activity by preventing its assembly into the elF4F complex. Mediates the regulation of protein translation by hormones, growth factors and other stimuli that signal through the MAP kinase pathway.
SUBUNIT: Nonphosphorylated Elf4EBP1 competes with Elf4G1/Elf4G3 to interact with Elf4E; insulin stimulated MAP-kinase (MAPK1 and
                                                                                                                                                                                     European
                                                                                                                                                                                                                                                                                                                                                                                         interact with EIF4E; insulin stimulated MAP-kinase (MAPKI and MAPK3) phosphorylation of EIF4EBP1 causes dissociation of the complex allowing EIF4G1/EIF4G3 to bind and consequent initiation of translation. Rapamycin can attenuate insulin stimulation,
; L36055; AAA622
; AB044548; BAB1
; BT007162; AAP3
; CR456769; CAG3
; BC004459; AAH0
; BC058073; AAH5
S50866; S50866.
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                                                                                                                                                                                     Swiss Institute
Bioinformatics
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                                                      BAB18650.
AAP35826.
CAG33050.
                   AAH04459.
AAH58073.
                                                                                                                                                                                     entry is copyright. It is produced through iss Institute of Bioinformatics and the EM oinformatics Institute. There are no restr
                                                                                                                                                                    content
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                                                                                                                                                                    is in no way
                                                                                                              mRNA.
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Listing first 45 summaries
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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   protein search, using
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Match Length
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1: /cgn2_6/ptcdata/1/iaa/5_COMB.pep:*

2: /cgn2_6/ptcdata/1/iaa/6_COMB.pep:*

3: /cgn2_6/ptcdata/1/iaa/H_COMB.pep:*

4: /cgn2_6/ptcdata/1/iaa/PCTUS_COMB.pep:*

5: /cgn2_6/ptcdata/1/iaa/RE_COMB.pep:*

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   BB
                 US-08-869-733-1
US-10-096-703-1
US-10-096-703-1
US-99-949-016-7744
US-08-869-733-3
US-09-215-063-3
US-09-215-063-3
US-10-096-703-4
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US-08-465-995A-2
US-08-465-994C-2
US-08-465-994C-2
US-08-465-994C-2
US-08-101-593-2
US-08-101-593-2
US-08-101-593-2
US-08-101-593-2
US-08-101-593-3
US-09-540-2368-5
US-09-134-000C-5685
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   Query Match 97.9%; Score 46; DB 1; Best Local Similarity 100.0%; Pred. No. 0.11; Matches 9; Conservative 0; Mismatches
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32 68.1 143 2 US-09-270-767-35637 32 68.1 143 2 US-09-854-122-43 32 68.1 361 2 US-09-854-122-43 32 68.1 362 2 US-09-854-122-42 32 68.1 362 2 US-09-854-122-42 32 68.1 501 2 US-09-158-767-15 32 68.1 501 2 US-09-158-767-17 32 68.1 501 2 US-09-158-767-18 32 68.1 501 2 US-09-158-767-18 32 68.1 501 2 US-09-158-767-18 32 68.1 501 2 US-09-113-794-16 32 68.1 501 2 US-09-13-794-16 32 68.1 501 2 US-09-713-794-17 32 68.1 501 2 US-09-713-794-18 32 68.1 501 2 US-09-713-794-18 32 68.1 501 2 US-09-713-794-18 32 68.1 501 2 US-09-713-794-18 32 68.1 505 2 US-09-713-794-18 32 68.1 505 2 US-09-713-794-18 32 68.1 505 2 US-09-713-794-18 32 68.1 505 2 US-09-713-794-18 32 68.1 505 2 US-09-713-794-18 32 68.1 505 2 US-09-713-794-18 32 68.1 505 2 US-09-713-794-18 32 68.1 505 2 US-09-713-794-18 32 68.1 505 2 US-09-713-794-18	45	44	43	42	. 41	40	39	38	37	36	3 5	34	ω ω	32	31	30	29	t
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US-09-270-767-35637 US-09-270-767-5854 US-09-854-122-43 US-09-854-122-42 US-09-248-796A-20723 US-09-158-767-15 US-09-158-767-17 US-09-158-767-17 US-09-158-767-18 US-09-158-767-17 US-09-158-767-17 US-09-1713-794-15 US-09-713-794-16 US-09-713-794-18 US-09-713-794-18 US-09-713-794-18 US-09-713-794-18 US-09-713-794-18 US-09-713-794-18 US-09-713-794-18 US-09-713-794-18 US-09-627-216A-12 US-09-627-216A-12 US-09-765-873A-12	N	N		N	N	N	N	N	N	N	N	N	N	N	N	N	N	
	US-09-854-122-44	US-09-765-873A-12	US-09-125-420A-22	US-09-627-216A-12	US-09-713-794-18	US-09-713-794-17	US-09-713-794-16	US-09-713-794-15	US-09-158-767-18	US-09-158-767-17	-	US-09-158-767-15	US-09-248-796A-20723	US-09-854-122-42	US-09-854-122-43	US-09-270-767-50854	US-09-270-767-35637	
	rddw 'th	יאליי יאלי		or Appl	•	•	•	15, App	-		16, Appi		2	42, App	•	50854, 4	3563/, A	

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US-08-869-733-1
US-08-869-733-1
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                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/869,733
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ELITATION ANDER:
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hillman, Jennifer L.
APPLICANT: Hawkins, Phillip R.
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NEW TRANSLATIONAL REGULATOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                   TOPOLOGY: line
IMMEDIATE SOURCE:
LIBRARY: BSTMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 3174 Por
CITY: Palo Alto
                                                                                               TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                        TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                    CLONE:
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                    805296
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3174 Porter Drive
                                         BSTMNOT01
                                                                               linear
                                                                                                 single
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Length 100; Indels

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RIIYDRKFL 45

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US-09-215-063-1
                                                                                      Sequence 1, Application US/10096703
Patent No. 6677126
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09215063
Patent No. 6365714
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/215,063

FILING DATE: 17-Dec-1998

CLASSIFICATION: «Unknown»

PRIOR APPLICATION NUMBER: 08/869,733

FILING DATE: «Unknown»

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0310 US

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                             Local Similarity 100.0%; | 108 | 9; Conservative 0;
                APPLICANT: Hillman, Jennifer L.
Hawkins, Phillip R.
TITLE OP INVENTION: NEW TRANSLATIONAL REGULATOR NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94304
COMPUTER READABLE FORM:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                              IMMEDIATE SOURCE:
LIBRARY: BSTMNOT01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hillman, Jennifer L.
Hawkins, Phillip R.
TITLE OF INVENTION: NEW TRANSLATIONAL REGULATOR NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                1 RIIYDRKFL 9
||||||||
37 RIIYDRKFL 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 100 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTMARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                CLONE: 805296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 415-845-4166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
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FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-90-08
NUMBER OF SEQ ID NOS: 207012
SOPTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 7744
LENGTH: 118
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Watches 9; Conserve
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                                         ) ORGANISM: Human
US-09-949-016-7744
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7744, Application US/09949016 Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
  Query Match
                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/215,063
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0310 US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: BOS
OPERATING SYSTEM: BOS
SOFTWARE: FBSTSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/10/096,703
FILING DATE: 12-Mar-2002
CLASSIFICATION: Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIBRARY: BSTMNOT01
CLONE: 805296
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: 11
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
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  97.9%;
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  Score 46;
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0.11;
DB 2;
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Length 118;
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RESULT 5
US-08-869-733-3
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                                                                                                        RESULT 6
US-08-869-733-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM COMPBELLAL
COMPUTER: IBM COMPBELLAL
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/869,733
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08869733
PAtent No. 5955278
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NEW TRANSLATIONAL REGULATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local
Matches
           Sequence 4, Application US/08869733
Patent No. 5955278
GENERAL INFORMATION:
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NEW TRANSLAY
                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                          STRANGE.
TOPOLOGY: 11...
IMMEDIATE SOURCE:
LIBRARY: GenBank
TONE: 561632
                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
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UMBER OF SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 3174 PO:
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 415-845-4166
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9; Conser
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Conservative (
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             Jennifer L.
Phillip R.
NEW TRANSLATIONAL REGULATOR
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; Mismatches
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RESULT 7
US-09-215-063-3
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Patent No. 6365714
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local Similarity 100.0%;
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OPERATING SYSTEM: DOS
SOPTWARE: FastSEQ for Windows Version 2.0
SCURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/869,733
FILING DATE: Herewith
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1658516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENGTH:
                 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTMARBE: FASTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/215,063
FILING DATE: 17-Dec-1998
CLASSIFICATION: <Unknown>
                                                                                                                                               ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hillman, Jennifer L.
Hawkins, Phillip R.
TITLE OF INVENTION: NEW TRANSLATIONAL REGULATOR
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 RITYDRKFL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RIIYDRKFL 9
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                                                                                                                                                                                                                        STATE: CA
                                                                                                                                                                                                       COUNTRY: USA
                                                                                                                                                                                                                                          CITY: Palo Alto
                                                                                                                                                                                                                                                             STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 amino acids
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RESULT 8
US-09-215-063-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/09215063
Patent No. 6365714
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
Hawkins, Phillip R.
TITLE OF INVENTION: NEW TRANSLATIONAL REGULATOR
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 97.9%; Score 46; DB 2; Best Local Similarity 100.0%; Pred. No. 0.13; Matches 9; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/869,733
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 749
REFERENCE/DOCKET NUMBER: PF-0310 US
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/215,063
FILING DATE: 17-Dec-1998
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/869,733 FILING DATE: <Unknown> ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                                                                                                                                  TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: CA
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LIBRARY: GenBank
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CLONE: 561632
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SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-096-703-3
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Patent No. 6677126
GENERAL INFORMATION:
                                                                Matches
                                                                              Query Match
Best Local
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Best Local S
                                                                                                                                                                                                                                                                                             TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/096,703
FILING DATE: 12-Mar-2002
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
                                                                                                                                                                                                                                                                                                                          NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0310 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hillman, Jennifer L.
Hawkins, Phillip R.
TITLE OF INVENTION: NEW TRANSLATIONAL REGULATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMMEDIATE SOURCE:
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51 RIIYDRKFL 59
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                                1 RIIYDRKFL 9
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Similarity 100.0%; Pred. No. 0.13;
9; Conservative 0; Miamatoho-
                                                                9
                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 09/215,063 FILING DATE: <Unknown>
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CLONE: 1658516
                                                                                                                                                                                                                              STRANDEDNESS: single
                                                                                                                                                                                                                                            TYPE: amino acid
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                                                                                                                                                                                                               TOPOLOGY:
                                                                Conservative
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                                                                                                                                                                                                               linear
                                                                              97.9%; Score 46; DB 2; 100.0%; Pred. No. 0.13;
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                                                                Mismatches
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RESULT 10

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US-10-096-703-4
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Patent No. 6677126
GENERAL INFORMATION:
Sequence 7860, Application US/09949016

Sequence 7860, Application US/09949016

PATENT NO. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
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Best Local Similarity 100.0%;
Matches 9; Conservative (
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 09/215,063
PILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0310 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPHONE: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/096,703
FILING DATE: 12-Mar-2002
CLASSIFICATION: CUnknown>
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COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: Incyte Pharmaceuticals, Inc.
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Hawkins, Phillip R.
TITLE OF INVENTION: NEW TRANSLATIONAL REGULATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIBRARY: GenBank
CLONE: 1658516
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 120 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 3174 Porter Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97.9%; Score 46; DB 2; 100.0%; Pred. No. 0.13;
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; ORGANISM: Human
US-09-949-016-7860
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US-08-465-995A-2
RESULT 13
US-08-465-995A-4
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SOPTWARE: FABLSEQ for Windows Version 4.0
SEQ ID NO 7860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 5660980
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Best Local Similarity
                                                                                                                                    Query Match 78.7%;
Best Local Similarity 75.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: ASCII DOS/TEXT
OPERATING SYSTEM: ASCII DOS/TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,995A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Robert Berliner
REGISTRATION NUMBER: 20,121
REFERENCE/DOCKET NUMBER: 1920-305D2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                TELEPHONE: 213/977-100
TELEFAX: 213/977-1003
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 90012-2628
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 898 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Myron F. Goodman
APPLICANT: Linda J. Reha-Krantz
TITLE OF INVENTION: METHODS FOR IDENTIFYING AND ISOLATING
TITLE OF INVENTION: VARIANT T4 POLYMERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Robbins, Berliner & Carson, LLP STREET: 201 No. 5660980th Figueroa Street, CITY: Los Angeles STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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99 IVYDRKFV 106
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                                                                                                                                                        Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                            1920-30502
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Sequence 4, Application US/08465995A Patent No. 5660980 GENERAL INFORMATION: APPLICANT: Myzon F. Goodman APPLICANT: Linda J. Reha-Krantz

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RESULT 14
US-08-465-994C-2
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 898 amino acids
TYPE: amino acid
TYPE: 11 near
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08465994C Patent No. 5928919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 78. Best Local Similarity 75. Matches 6; Conservative
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
OPERATING SYSTEM: ASCII DOS/TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,994C
FILING DATE: 06-UN-1995
CILASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MARCARET A. CHURCHILL
REGISTRATION NUMBER: 39,944
REFERENCE/DOCKET NUMBER: 1920-305D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 213/977-1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: ASCII DOS/TEXT CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/465,995A
                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Robbins, Berliner & Carson, LLP
STREET: 201 No. 5928919th Figueroa Street,
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Robert Berliner
REGISTRATION NUMBER: 20,121
REFERENCE/OCKET NUMBER: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 213/977-1001
TELEFAX: 213/977-1003
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Robbins, Berliner & Carson, LLP
STREET: 201 No. 5660980th Figueroa Street, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: MYRON F. APPLICANT: LINDA L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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CITY: LOB Angeles
STATE: California
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CLASSIFICATION: 435
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|VYDRKFV 106
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75.0%;
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Search completed: November 29, 2005, 23:04:22 Job time: 24.8636 secs
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                                                                                                                     Matches
                                                                                                                                    Query Match
Best Local 9
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LINDA L. REHA-KRANTZ
TITLE OF INVENTION: VARIANT DNA POLYMERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 6; Conserv
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: ISM PC compatible
OPERATING SYSTEM: ASCII DOS/TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,994
                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 39,944
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: MARGARET A. CHURCHILL
REGISTRATION NUMBER: 39,944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Robbins, Berliner & Carson, LLP
STREET: 201 No. 5928919th Figueroa Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: protein
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                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Los Angeles
STATE: California
                                                                                                                                                                                                               TOPOLOGY:
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CLASSIFICATION: 435
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99 IVYDRKFV 106
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amino acid
XGY: linear
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|VYDRKFV 106
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                                                                                                                     Conservative
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75.0%;
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75.0%;
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                                                                                                                     2;
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                                                                                                                                    Score 37;
Pred. No.
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                                                                                                                      Mismatches
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Perfect score:
                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      November 29, 2005, 22:52:34; Search time 77.9545 Seconds (without alignments) 53.599 Million cell updates/sec
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                                                                                                           Published Applications AA Main:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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## SUMMARIES

27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	თ	ហ	4.	w	N	_	Regult No.
34	ω 4	34	34	34	35	35	35	35	37	38	39	41	42	46	46	46	46	46	46	46	46	46	46	46	46	46	Score
72.3	•	•	•	•	74.5		•	•	78.7	٠	•	87.2	٠	97.9	•	•	•	•	•	97.9	•	•	•	•	•	97.9	Query Match
500	484	223	16	16	1679	1679	977	105	898	128	16	9	63	138	120	120	119	118	118	117	100	100	16	16	16	9	Length
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-10-425-115	-10-425-114-4950	US-11-097-143-24573	US-09-973-473-17	-473-		US-11-097-143-8286	US-10-425-115-272448	1		US-10-210-281-68	US-09-973-473-15	US-10-353-929-15	US-10-425-115-251396		US-10-096-703-4	US-10-096-703-3	US-09-925-300-1267	US-10-631-467-917	US-10-353-929-48	US-10-631-467-1617	US-10-408-765A-416	-703-	US-09-973-473-8		9	US-10-353-929-14	ID
	Sequence 49505, A	245	17,	16,		,	272448	27245	ø	68, 7	e 15,	15,	æ	e L	Sequence 4, Appli	Sequence 3, Appli	e 126	e 917,	e 48, F	e 1617,		e 1, Ar	e 8,	е 7,	Sequence 6, Appli	4	Description

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28
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US-10-425-115-271286	US-10-425-115-290615	US-10-425-115-303877	US-10-425-115-291856	US-10-282-122A-53037	US-10-504-543-4	US-10-425-115-267141	US-10-282-122A-66350	US-10-767-701-48906	US-10-425-115-364979	US-10-767-701-35373	US-10-282-122A-42947	US-10-424-599-175084	US-10-425-115-185633	US-10-437-963-187680	US-10-437-963-187691	US-10-424-599-189465	US-10-732-923-16954
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
271286,	290615,	303877,	291856,	53037, A	4, Appli	267141,	66350, A	48906, A	364979,	35373, A	42947, A	175084,	185633,	187680,	187691,	189465,	16954, A

## ALIGNMENTS

RESULT 1 US-10-353-929-14

Sequence 14, Application US/10353929 Publication No. US20030175288A1 GENERAL INFORMATION:

FILE REFERENCE: GP01-1024
FILE REFERENCE: GP01-1024
CURRENT APPLICATION NUMBER: US/10/353,929
CURRENT FILING DATE: 2003-01-30
PRIOR APPLICATION NUMBER: JP P2000-231814
PRIOR PILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 197
SOFTWARE: Patentin version 3.1
SEQ ID NO 14
LENGTH: OATE: AVOID NOS: 197

LENGTH: 9 TYPE: PRT

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Sequence 6, Application US/09973473

; Sequence 6, Application No. US20030041341A1

; GENERAL INFORMATION:
   APPLICANT: SOMENBERG, Nahum
   APPLICANT: TREMBLAY, Michel
   APPLICANT: TRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
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Best Local Similarity
Thes 9; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-353-929-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial
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Conservative 0;
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100.0%; Pred. No. 1.
ive 0; Mismatches
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o. 1.7e+06;
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Query Match
Best Local Similarity
Matches 9; Conserve
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-973-473-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/09973473
Publication No. US20030041341A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/09973473 Publication No. US20030041341A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 16
TYPE: PRT
APPLICANT: SONENBERG, Nahum
APPLICANT: TREMBLAY, MICHE!
APPLICANT: TREMBLAY, MICHE!
APPLICANT: TSUKIAYAMA-KOHARA, KYOKO
TITLE OF INVENTION: NON-HUMAN TRANSGENIC ANIMAL WHOSE GERM CELLS AND
TITLE OF INVENTION: SOMATIC CELLS CONTAIN A KNOCKOUT MUTATION IN DNA
TITLE OF INVENTION: ENCODING 4E-BP1
FILE REFERENCE: 514012000400
CURRENT APPLICATION NUMBER: US/09/973,473
CURRENT FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: PCT/CA00/00388
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 60/128,559
                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo gapiens -09-973-473-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SONENBERG, Nahum
APPLICANT: TREMBLAY, MiSchel
APPLICANT: TREMBLAY, MISCHEl
APPLICANT: TSUKIAYAMA-KOHARA, KYOKO
TITLE OF INVENTION: NON-HUMAN TRANSCENIC ANIMAL WHOSE GERM CEILS AND
TITLE OF INVENTION: SOMATIC CELLS CONTAIN A KNOCKOUT MUTATION IN DNA
TITLE OF INVENTION: SOMATIC CELLS CONTAIN A KNOCKOUT MUTATION IN DNA
FILE REFERENCE: 514012000400
CURRENT APPLICATION NUMBER: US/09/973,473
CURRENT APPLICATION NUMBER: DOT/CA00/00388
PRIOR APPLICATION NUMBER: PCT/CA00/00388
PRIOR APPLICATION NUMBER: 60/128,559
PRIOR APPLICATION NUMBER: 60/128,559
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 1999-04-09
PRIOR FILING DATE: 1999-04-09
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PRIOR FILING DATE: 2000-02-02
NUMBER OF SEQ ID NOS: 27
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PRIOR FILING DATE: 2000-02-02
NUMBER OF SEQ ID NOS: 27
SOPTWARE: Patentin Ver. 2.1
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Local Similarity 100.0%; Pred. No.
hes 9; Conservative 0; Mismatci
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0.044;
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Query Match
Best Local Similarity
Thes 9; Conserve
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Best Local Similarity
Thes 9; Conserve
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US-10-096-703-1
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PRIOR APPLICATION NUMBER: 60/179,743
PRIOR FILING DATE: 2000-02-02
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/10096703
Publication No. US20020132330A1
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer
                                                                                                                                                                                                                                                      TELEFAX: 415-845-4166
TELEX: <UNKNOWN>
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/215,063
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: COMPATION:

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTMARE: FASTUSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/096,703
FILING DATE: 12-Mar-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: PF-0310 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                          SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hawkins, Phillip R.
TITLE OF INVENTION: NEW TRANSLATIONAL REGULATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RIIYDRKFL 9
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                               LIBRARY: BSTMNOT01
CLONE: 805296
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                 Conservative
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Hawkins, Phillip R.
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                                  97.9%; Score 46;
100.0%; Pred. No.
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                 0; Mismatches
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                                  DB 4;
0.29;
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1 RIIYDRKFL 9

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RESULT 7
US-10-631-467-1617
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-416
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Best Local Similarity
Warches 9; Conserva
RESULT 8
US-10-353-929-48
/ Sequence 48, Application US/10353929
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US-10-631-467-1617
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FILE REFERENCE: 3462.1005-000
CURRENT APPLICATION NUMBER: US/10/631,467
CURRENT FILING DATE: 2003-07-31
PRIOR APPLICATION NUMBER: JP 2003-077212
PRIOR FILING DATE: 2003-03-20
PRIOR FILING DATE: 2003-03-20
PRIOR FILING DATE: 2002-08-06
NUMBER OF SEQ ID NOS: 2086
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CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOPTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 416
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Publication No. US20040101874A1
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Best Local Similarity
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APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale E.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
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APPLICANT: Fahy, Eoin D.
APPLICANT: Zhang, Bing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Genox Research Inc.
TITLE OF INVENTION: Method for testing for broncheal asthma, or chronic obstructive
TITLE OF INVENTION: disease
                                                                                                                                                                                                                                                                                                         LENGTH: 117
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PRIOR APPLICATION NUMBER: JP P2000-231814
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 197
SOFTWARE: Patentin version 3.1
SEQ ID NO 48
LENGTH: 118
TYPE: PRT
ORGANISM: Homo sapiens
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US-10-631-467-917
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US-10-631-467-917
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US-09-925-300-1267
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CURRENT APPLICATION NUMBER: US/10/631,467
CURRENT FILING DATE: 2003-07-31
PRIOR APPLICATION NUMBER: JP 2003-077212
PRIOR FILING DATE: 2003-03-20
PRIOR FILING DATE: 2003-03-09
PRIOR FILING DATE: 2003-08-06
PRIOR FILING DATE: 2002-08-06
NUMBER OF SEQ ID NOS: 2086
GENERAL INFORMATION:

APPLICANT: Craig Rosen,
APPLICANT: Steve Ruben
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT PILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR APPLICATION NUMBER: 60/124,270
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SEQ ID NO 917
LENGTH: 118
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TITLE OF INVENTION: Method for testing for broncheal asthma, or chronic obstructive $
TITLE OF INVENTION: disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: ITOH, Kyogo
TITLE OF INVENTION: Tumor antigen
FILE REFERENCE: GP01-1024
CURRENT APPLICATION NUMBER: US/10/353,929
CURRENT FILING DATE: 2003-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
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Local Similarity 100.0%;
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Pred. No.
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US-09-925-300-1267
                                                                                                                                       US-10-096-703-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/10096703
Publication No. US20020132330A1
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
Hawkins, Phillip R.
TITLE OF INVENTION: NEW TRANSLATIONAL REGULATOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver.
SEQ ID NO 1267
LENGTH: 119
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                                                                                    Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 1890
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                           TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                             NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0310 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/215,063
FILING DATE: <UNknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94304
COMPUTER READABLE FORM:
                                                                                                                                                         SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FASTSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                          IMMEDIATE SOURCE:
51
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                                                                                    Similarity
                                  RIIYDRKFL 9
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RIIYDRKFL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/10/096,703
FILING DATE: 12-Mar-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                       LIBRARY: GenBank CLONE: 561632
                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 3174 Porter Drive CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: CA
                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                            LENGTH: 120 amino acide
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                                                                    Conservative
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                                                                                  97.9%; Score 46; DB 4; Length 120; 100.0%; Pred. No. 0.34;
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US-09-925-301-1164

; Sequence 1164, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR RILING DATE: 2000-03-08
; PRIOR FILING DATE: 1090-03-18
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR APPLICATION NUMBER: 60/124,270
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Best Local
TUMBER OF SEQ ID NOS: 1694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 09/215,063
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: PF-0310 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/10/096,703
FILING DATE: 12-Max-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLONE: 1658516
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hawkins, Phillip R.
TITLE OF INVENTION: NEW TRANSLATIONAL REGULATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                51 RIIYDRKFL 59
                                                                                                                                                                                                                                                                                                                                                    1 RIIYDRKFL 9
                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 120 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 415-845-4166
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RESULT 14
US-10-425-115-251396, Application US/10425115
; Sequence 251396, Application US/10425115
; Publication No. US20040214272A1
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 251396
; LENGTH: 63
                                                                                                                   RESULT 15
US-10-353-929-15
Sequence 15, Application US/10353929
Publication No. US20030175288A1
GENERAL INFORMATION:
APPLICANT: ITOH, Kyogo
TITLE OF INVENTION: Tumor antigen
FILE REFERENCE: GP01-1024
CURRENT APPLICATION NUMBER: US/10/353,929
CURRENT FILING DATE: 2003-01-30
PRIOR APPLICATION NUMBER: JP P2000-231814
PRIOR PILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 197
SOPTWARE: PatentIn version 3.1
SEQ ID NO 15
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, ORGANISM: Homo sapiens
US-09-925-301-1164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) OTHER INFORMATION: Clone ID: MRT4577_160859C.1.pep US-10-425-115-251396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1164
LENGTH: 138
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Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 9; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 89.4%; Score 42; DB 4; Length 63; Best Local Similarity 88.9%; Pred. No. 1.1; Matches 8; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(63)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PF
                                                      LENGTH: 9
TYPE: PRT
ORGANISM: Artificial
OTHER INFORMATION: Designed peptide having an ability to activate HLA-A2 restricted OTHER INFORMATION: Cytotoxic T lymphocytes
                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 RITYDRKFL 79
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US-10-353-929-15
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Best Local Similarity
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                              8; Conservative
                              87.2%; Score 41; DB 4; Length 9; 100.0%; Pred. No. 1.7e+06; tive 0; Mismatches 0; Indels
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                                   Gaps
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Search completed: November 29, Job time: 78.9545 secs 2005, 23:10:28

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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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      protein search, using
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1: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-667-295-139
US-10-667-295-139
US-11-065-943-52
US-11-065-943-52
US-11-022-562-278
US-11-023-626-3174
US-10-93-626-3174
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US-10-821-234-915
US-10-821-234-1581
US-10-821-234-1581
US-10-821-234-1581
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US-10-924-820A-12
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12.124 Million cell updates/sec
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Sequence 83, Appl
Sequence 82, Appl
Sequence 140, App
Sequence 139, App
Sequence 52, Appl
Sequence 52, Appl
Sequence 2774, Ap
Sequence 2774, Ap
Sequence 3174, Ap
Sequence 1915, App
Sequence 1581, App
Sequence 1581, App
Sequence 16, Appl
Sequence 16, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 17, Appli
Sequence 8, Appli
Sequence 17, Appli
Sequence 212, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                          Description
   Sequence 141, Application US/10667295

Publication No. US20050257293A1

GENERAL INFORMATION:

APPLICANT: Mascia, Peter

ITILE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM

FILE REFERENCE: 11696-047001

CURRENT APPLICATION NUMBER: US/10/667,295

CURRENT FILING DATE: 2003-09-17

PRIOR APPLICATION NUMBER: US 60/411,823

PRIOR APPLICATION NUMBER: US 60/411,823

PRIOR FILING DATE: 2002-09-17

NUMBER OF SEQ ID NOS: 263

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 141
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US-10-667-295-141
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45	44	43	42	41	40	39	96	37	36	35 5	34	33	32	31	30	29	28	27	26
26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26
55.3	55.3	55.3	55.3	55.3	55.3	55.3	55.3	55.3	55.3	55.3	55.3	55.3	55.3	55.3	55.3	55.3	55.3	55.3	55.3
1338	1338	1189	1170	1094	770	770	709	698	683	654	651	591	505	354	354	321	310	309	309
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US-11-109-156-23	US-10-821-234-1622	-234	US-10-858-730-71	US-10-821-234-1097	US-10-789-273-38	US-10-982-545-15	US-11-074-176-158	US-10-793-626-2388	US-11-046-668-2	US-11-046-668-4	US-10-994-820A-34	US-10-485-517-332	US-10-519-447-4	US-10-485-517-366	US-10-485-517-179	US-10-793-626-2816	US-10-994-820A-10	US-10-994-820A-2	US-10-485-517-161
Sequence 23, Appl	1622	-			Sequence 38, Appl	Sequence 15, Appl	•	2388		•	•	332	4, A	sequence 366, App	1,4	287	E 10, AL		16

ALIGNMENTS

## ; LENGTH: 433 ; TYPE: PRT ; ORGANISM: Arabidopsis thaliana ; FEATURE: ; NAME/KEY: VARIANT ; LOCATION: (1)...(433) ; OTHER INFORMATION: Ceres Seq. ID US-10-667-295-83 RESULT 1 US-10-667-295-83 Sequence 83, Application US/10667295 ; Publication No. US20050257293A1 ; GENERAL INFORMATION: ; APPLICANT: MASCIA, Peter ; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT ; FILE REFERENCE: 11696-047001 NUMBER OF SEQ ID NOS: 263 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 83 CURRENT APPLICATION NUMBER: US/10/667,295 CURRENT FILING DATE: 2003-09-17 PRIOR APPLICATION NUMBER: US 60/411,823 PRIOR FILING DATE: 2002-09-17 Local Similarity tes 5; Conserv **116 RIMFDRRF 123** 1 RIIYDRKF 8 Conservative 68.1%; 62.5%; Score 32; Pred. No. ä no. Mismatches 12558792 DB 1; 7.2; SYSTEM 0 Length 433; Indels <u>,</u> Gaps

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Sequence 140, Application US/10667295
Publication No. US20050257293A1
GENERAL INFORMATION:
APPLICANT: Mascia, Peter
TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
FILE REFERENCE: 11696-047001
CURRENT APPLICATION UNMBER: US/10/667,295
CURRENT FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: US 60/411,823
PRIOR PILING DATE: 2002-09-17
NUMBER OF SEQ ID NOS: 263
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Glycine max
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(434)
OTHER INFORMATION: Ceres Seq. ID no. 13531808
US-10-667-295-141
                                                                                                                                                                                                                                                                                                                                                                                       US-10-667-295-140
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; NAME/KEY: VARIANT
; LOCATION: (1)...(505)
; OTHER INFORMATION: Ceres Seq. ID no. 12558791
US-10-667-295-82
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LENGTH: 505
TYPE: PRT
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Matches
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Publication No. US20050257293A1
GENERAL INFORMATION:
APPLICANT: MASCIA, Peter
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/667,295
CURRENT FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: US 60/411,823
PRIOR FILING DATE: 2002-09-17
NUMBER OF SEQ ID NOS: 263
SOFTWARE: FBSESEQ for Windows Version 4.0
ORGANISM: Glycine max
FORTURE:
NAMEJ/KEY: VARIANT
LOCATION: (1)...(506)
OTHER INFORMATION: Ceres Seq. ID no. 13531807
                                                                                                    TYPE: PRT
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                                                                                                                     ENGTH: 506
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Similarity 62.5%;
5; Conservative
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Pred. No. 8.3;
3; Mismatches
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APPLICANT: MASCIA, Peter
TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
FILE REFERENCE: 11696-047001
CURRENT APPLICATION NUMBER: US/10/667,295
CURRENT FILING DATE: 2003-09-17
FRIOR APPLICATION NUMBER: US 60/411,823
PRIOR FILING DATE: 2002-09-17
NUMBER OF SEQ ID NOS: 263
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 139
LENGTH: 526
                                                                                                                                                                                   APPLICANT: MASCIA, Peter
TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
FILE REFERENCE: 11696-047001
CURRENT APPLICATION NUMBER: US/10/667,295
CURRENT FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: US 60/411,823
PRIOR FILING DATE: 2002-09-17
INUMBER OF SEQ ID NOS: 263
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 81
SEQ ID NO 81
Query Match
Best Local Similarity
Watches 5; Conserve
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Best Local Similarity
Watches 5; Conserve
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, NAME/KEY: VARIANT
, LOCATION: (1)...(526)
, OTHER INFORMATION: Ceres Seq. ID no. 13531806
US-10-667-295-139
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                                                                            US-10-667-295-81
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Matches 5; Conserv
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                                                                                PEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(334)
OTHER INFORMATION: Ceres Seq. ID no. 12558790
                                                                                                                                                   TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Glycine max
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o. US20050257293A1
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              Conservative
                            68.1%;
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              3; Mismatches
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Pred. No.
                            Score 32; L
Pred. No. 8.
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Pred. No. 8.4;
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                                           DB 1;
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9.7;
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                                            Length 534;
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                Indels
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1 RIIYDRKF 8

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PRIOR APPLICATION NUMBER: PCT/US03/20322
PRIOR FILING DATE: 2003-06-27
PRIOR APPLICATION NUMBER: 60/392718
PRIOR FILING DATE: 2002-06-27
NUMBER OF SEQ ID NOS: 340
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 228
LENGTH: 396
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; TYPE: PRT
; ORGANISM: Bacillus circulans
US-11-065-943-52
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US-11-022-562-228
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RESULT 9
US-10-793-626-2774
; Sequence 2774, Application US/10793626
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                                                                                                                                                          Query Match
Best Local Similarity
Finds 5; Conserve
                                                                                                                                                                                                                                                         ; TYPE: PRT ; ORGANISM: Clostridium difficile US-11-022-562-228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 228, Application US/11022562 Publication No. US20050249742A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:

APPLICANT: JESTIN, JEAN-LUC

APPLICANT: VICHLER-GUERRE, SOPHIE

APPLICANT: FERRIS, STEPHANE

APPLICANT: FERRIS, STEPHANE

TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I

TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,

TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 52, Application US/11065943 Publication No. US20050250131A1
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CURRENT APPLICATION NUMBER: US/11/065,943
CURRENT FILING DATE: 2005-02-25
PRIOR APPLICATION NUMBER: US 10/787,219
PRIOR PILING DATE: 2004-02-27
NUMBER OF SEQ ID NOS: 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ruprecht, Ruth M.
APPLICANT: Shisong, Jiang
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONS
FILE REFERENCE: DFN-043CN
CURRENT APPLICATION NUMBER: US/11/022,562
CURRENT FILING DATE: 2004-12-22
CURRENT FILING DATE: 2004-12-22
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                                                                                                                                                                            Conservative
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Pred. No. 18;
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Pred. No. 41;
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Sequence 3174, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT FILING DATE: 2004-03-04
; CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3174
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
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OTHER INFORMATION: Description of Artificial Sequence: synthetic;
OTHER INFORMATION: amino acid sequence
US-10-793-626-2774
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US-10-793-626-3174
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PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2774
                 Sequence 915, Application US/10821234

Publication No. US20050255114A1

GENERAL INFORMATION:

APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
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TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PUJ480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
                                                                                                                                                                                                                                                                                                                                                                                          Matches
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CURRENT APPLICATION NUMBER: US/10/821,234
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TYPE: PRT
ORGANISM: Artificial Sequence
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Local Similarity 83.3%;
les 5; Conservative
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                          4.
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Pred. No. 44;
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US-10-821-234-1581
, Sequence 1581, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
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CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR FILING DATE: 2004-02-11
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR FILING DATE: 2002-11-14
PRIOR FILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-11-16
PRIOR PRILING DATE: 2001-12-19
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
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; ORGANISM: Homo sapiens
US-10-821-234-915
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LENGTH: 251
TYPE: PRT
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PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt_SEQ_genes Version 1.0
SEQ ID NO 915
LENGTH: 478
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Publication No. US20
GENERAL INFORMATION:
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Matches 5; Conserv
                                                                                                                                                                                                                                                                                                Query Match
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PRIOR FILING DATE: 2000-10-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
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Local Similarity 66.7%;
hes 6; Conservative
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83.3%;
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Pred. No. 41;
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Pred. No. 49;
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APPLICANT: CHARGE AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C128
CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
PRIOR APPLICATION NUMBER: 60/049911
PRIOR APPLICATION NUMBER: 60/05974
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/059113
PRIOR APPLICATION NUMBER: 60/059115
PRIOR APPLICATION NUMBER: 60/059117
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/05912
PRIOR APPLICATION NUMBER: 60/059184
PRIOR APPLICATION NUMBER: 60/059263
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-19
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059352
PRIOR APPLICATION NUMBER: 60/059352
PRIOR APPLICATION NUMBER: 60/059352
PRIOR APPLICATION NUMBER: 60/059352
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Best Local Similarity
'hes 6; Conserv
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US-10-131-826A-452
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SEQ ID NO 1581
LENCTH: 402
TYPE: PRT
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APPLICANT:
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PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
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CURRENT FILING DATE: 2004-04-07
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TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
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Watanabe, Colin K
Wood, William
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sherwood, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gurney, Austin L.
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Godowski, Paul J.
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Andarmani, Susan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stewart, Timothy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Beresini, Maureen
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75.0%;
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Pred. No.
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APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Stache-Crain, Susan
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
CURRENT APPLICATION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOPTWARE: pt_SEQ_genes Version 1.0
SEQ ID NO 1083
LENGTH: 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Remaining Prior Application data removed - See File Wrapper or PALM.; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 452
; ENGTH: 477
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-452
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; ORGANISM: Homo sapiens
; PEATURE;
; NAME/KEY: misc_feature
; LOCATION: (1)...(1150)
; OTHER INFORMATION: Xaa = any amino acid or nothing
US-10-821-234-1083
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Search completed: November 29, 2005, 23:04:38 Job time : 2.75 secs
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Best Local Similarity 55.6%;
Matches 5; Conservative
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1008 QMIYQRPFL 1016
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Pred. No. 1.9e+02;
2; Mismatches 2; Indels
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Result
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Perfect score:
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ALIGNMENTS

## RESULT 1 ABP83755 CCCCCCXxxxqqqqxqxqxxqxxqxxqxxqxx Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH; humoral immune response; cellular immune response; suppression subtractive hybridisation; HLA; human leukocyte antigen. ABP83755 standard; peptide; 9 AA. WO200283068-A2 Homo sapiens. HLA protein 121P2A3 28-MAR-2003 ABP83755; 24-OCT-2002. (first entry) peptide #110.

## Challita-Eid PM, R Afar DEH, Saffran 10-APR-2001; 2001US-0282739P. 25-APR-2001; 2001US-0286630P. 22-JUN-2001; 2001US-0300373P. 09-APR-2002; 2002WO-US011359. (AGEN-) AGENSYS INC. Raitano AB, 'n Morrison Faris n K, M Morrison RK, c RS, Mitchell SC; W, Jakobovit Jakobovits A;

New composition comprising a substance that modulates the status of 121P2A3 polypeptides, useful for eliciting humoral or cellular immune responses or in assessing the status of 121P2A3 gene products in normal WPI; 2003-092956/08.

Claim 13; Page 130; 362pp; English.

versus cancerous tissues.

The invention relates to a novel composition comprising a substance that modulates the status of a protein, 121P2A3. The composition of the invention has cytostatic and immunostimulant activity, and is useful as a vaccine. The 121P2A3 proteins and polynucleotides are useful for eliciting humoral or cellular immune response. The polynucleotides are useful for characterising cytogenetic abnormalities of this chromosomal locus, as tools that can be used to delineate cytogenetic abnormalities

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invention has cytostatic and immunostimulant activity, and is useful as a vaccine. The 12192A3 proteins and polynucleotides are useful for eliciting humoral or cellular immune response. The polynucleotides are useful for characterising cytogenetic abnormalities of this chromosomal locus, as tools that can be used to delineate cytogenetic abnormalities in the chromosomal region that encodes 12192A3 that may contribute to malignant phenotype, and in assessing the status of 12192A3 gene products in normal versus cancerous tissues. The proteins are useful for generating and characterising domain-specific antibodies, for identifying
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New composition comprising a substance that modulates the status of 121P2A3 polypeptides, useful for eliciting humoral or cellular immune responses or in assessing the status of 121P2A3 gene products in norms
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Afar DEH, Saffran
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                     The invention relates to a novel composition comprising a substance that modulates the status of a protein, 121223. The composition of the invention has cytostatic and immunostimulant activity, and is useful as a vaccine. The 121223 proteins and polynucleotides are useful for eliciting humoral or cellular immune response. The polynucleotides are useful for composition that can be used to delineate cytogenetic abnormalities in the chromosomal region that encodes 121223 that may contribute to malignant phenotype, and in assessing the status of 121223 gene products in normal versus cancerous tissues. The proteins are useful for generating and characterising domain-specific antibodies, for identifying agents or cellular factors that bind to 121223 or a particular structure domain, and in various therapeutic and diagnostic contexts, including cancer vaccines. The antibodies or cells reactive with the product are
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New composition comprising a substance that modulates the status 121P2A3 polypeptides, useful for eliciting humoral or cellular in responses or in assessing the status of 121P2A3 gene products in versus cancerous tissues.
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                                        The invention relates to a novel composition comprising a substance that CC modulates the status of a protein, 121P2A3. The composition of the CC invention has cytostatic and immunostimulant activity, and is useful as a CC vaccine. The 121P2A3 proteins and polynucleotides are useful for celiciting humoral or cellular immune response. The polynucleotides are CC useful for characterising cytosenetic abnormalities of this chromosomal CC locue, as tools that can be used to delineate cytosenetic abnormalities of the chromosomal region that encodes 121P2A3 that may contribute to CC malignant phenotype, and in assessing the status of 121P2A3 gene products in normal versus cancerous tissues. The proteins are useful for CC agents or cellular factors that bind to 121P2A3 or a particular structure CC domain, and in various therapeutic and diagnostic contexts, including CC cancer vaccines. The antibodies or T cells reactive with the product are useful in passive or active immunisation, and in imaging methodologies CC for the management of cancer. The sequences shown in ABB83646 - ABB95595
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25-APR-2001; 2001US-0286630P.
22-JUN-2001; 2001US-0300373P.
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                                peptides from the 121P2A3 variants of the invention
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Pred. No. 2e+06;
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n K, Morrison RK,
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W, Jakobovi
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                          The invention relates to a novel composition comprising a substance that CC modulates the status of a protein, 121P2A3. The composition of the CC invention has cytostatic and immunostimulant activity, and is useful as a CC vaccine. The 121P2A3 proteins and polymucleotides are useful for CC eliciting humoral or cellular immune response. The polymucleotides are CC useful for characterising cytogenetic abnormalities of this chromosomal locus, as tools that can be used to delineate cytogenetic abnormalities in he chromosomal region that encodes 121P2A3 that may contribute to CC malignant phenotype, and in assessing the status of 121P2A3 gene products in normal versus cancerous tissues. The proteins are useful for CC generating and characterising domain-specific antibodies, for identifying CC agents or cellular factors that bind to 121P2A3 or a particular structure domain, and in various therapeutic and diagnostic contexts, including CC cancer vaccines. The antibodies or T cells reactive with the product are useful in passive or active immunisation, and in imaging methodologies for the management of cancer. The sequences shown in ABP8364 - ABP95595 CC represent peptides from the 121P2A3 variants of the invention
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Matches 2
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25-APR-2001; 2001US-0286630P.
22-JUN-2001; 2001US-0300373P.
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                                                                                                                                                                                                                                                                                                                                                                 New composition comprising a substance that modulates the status of 121P2A3 polypeptides, useful for eliciting humoral or cellular immune responses or in assessing the status of 121P2A3 gene products in normal
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n D, Morrison K, N
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Pred. No. 2e+0
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cison RK,
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                                                                                                                                                                                                                                                                                        The invention relates to a novel composition comprising a substance that modulates the status of a protein, 12122A3. The composition of the invention has cycostatic and immunostimulant activity, and is useful as a vaccine. The 1212A3 proteins and polynuclectides are useful for callular immune response. The polynuclectides are useful for characterising cytogenetic abnormalities of this chromosomal locus, as tools that can be used to delineate cytogenetic abnormalities in the chromosomal region that encodes 1212A3 that may contribute to malignant phenotype, and in assessing the status of 1212PA3 gene products in normal versus cancerous tissues. The proteins are useful for generating and characterising domain-specific antibodies, for identifying agent or cellular factors that bind to 1212A3 or a particular structure domain, and in various therapeutic and diagnostic contexts, including cancer vaccines. The antibodies or T cells reactive with the product are useful in passive or active immunisation, and in imaging methodologies for the management of cancer. The sequences shown in ABP83646 - ABP995595 represent peptides from the 1212PA3 variants of the invention
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Matches 2
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22-JUN-2001; 2001US-0300373P
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Afar DEH, Saffran
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n D, Morrison
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Pred. No. 2e+06;
0; Mismatches
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25-APR-2001; 2001US-0286630F
22-JUN-2001; 2001US-0300373F
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YSTTTL 8
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RESULT 8

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22-JUN-2001; 2001US-0300373P.
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                ABP87077;
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                                                 ABP87077 standard; peptide; 9 AA
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33.3%;
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Pred. No. 2e+06;
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Morrison RK, Ge
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Best Local Similarity
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25-APR-2001;
22-JUN-2001;
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Afar DEH, Saffran D,
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               HLA protein 121P2A3 peptide #5262
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Morrison K, Morrison RK, Ge
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             Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH; humoral immune response; cellular immune response; suppression subtractive hybridisation; HLA; human leukocyte antigen
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Afar DEH, Saffran
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25-APR-2001; 2001US-0286630P.
22-JUN-2001; 2001US-0300373P.
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n D, Morrison
                                                                                                                           entry)
                                                                                     peptide
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Pred. No. 2e+06;
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Morrison RK, Ge
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RESULT 12
ABP84056
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Best Local
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25-APR-2001; 2001US-0286630P
22-JUN-2001; 2001US-0300373P
                                                                                      Homo sapiens.
                                                                                                                                     suppression subtractive hybridisation;
                                                                                                                                                                      Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH; humoral immune response; cellular immune response;
                                                                                                                                                                                                                                                         HLA protein 121P2A3 peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                   ABP84056 standard;
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2; Conserv
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                                                                                                                                        response; cellular immune res
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                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide; 9
                                                                                                                                                                                                                                                                                                                     entry)
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Pred. No.
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on K, Morr
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LA; human
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                                                                                                                                              leukocyte
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W, Jakobovi
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RESULT 13
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cc modulates the status of a protein, 12122A3. The composition of the convention has cytostatic and immunostimulant activity, and is useful as a cc vaccine. The 1212A3 proteins and polynucleotides are useful for calcular immune response. The polynucleotides are cc eliciting humoral or cellular immune response. The polynucleotides are cc useful for characterising cytogenetic abnormalities of this chromosomal colors, as tools that can be used to delineate cytogenetic abnormalities cc in the chromosomal region that encodes 1212A3 that may contribute to cc malignant phenotype, and in assessing the status of 1212A3 gene products cl normal versus cancerous tissues. The proteins are useful for cg generating and characterising domain-specific antibodies, for identifying cagents or cellular factors that bind to 1212A3 or a particular structure domain, and in various therapeutic and diagnostic contexts, including cc cancer vaccines. The antibodies or T cells reactive with the product are cuseful in passive or active immunisation, and in imaging methodologies cor the management of cancer. The sequences shown in ABP83646 - ABP95595 cc represent peptides from the 1212PA3 variants of the invention
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Best Local Similarity
Matches 2; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 13; Page 136; 362pp; English
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25-APR-2001;
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                                                                                                                                         Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH; humoral immune response; cellular immune response; suppression subtractive hybridisation; HLA; human leukocyte antigen.
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                                                                                                                                                                                                            HLA protein 121P2A3
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                                                                                                                                                                                                                                                                                                             ABP84643 standard; peptide; 9 AA.
               09-APR-2002; 2002WO-US011359.
                                               24-OCT-2002
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Saffran
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2001US-0286630P.
2001US-0300373P.
                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                            peptide #998.
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Morrison K, Morrison
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2e+06;
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W, Jakobovi
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RESULT 14
ABP85166
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Best Local S
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Afar DEH, Saffran D,
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25-APR-2001; 2001US-0286630P.
22-JUN-2001; 2001US-0300373P.
                                                                                                                                                                                                          Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH; humoral immune response; cellular immune response; suppression subtractive hybridisation; HLA; human leukocyte antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 13; Page 147; 362pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           versus cancerous tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-092956/08
             10-APR-2001; 2001US-0282739P.
25-APR-2001; 2001US-0286630P.
22-JUN-2001; 2001US-0300373P.
                                                                                                                                                                                                                                                                          HLA protein 121P2A3 peptide #1521.
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                                                                               09-APR-2002; 2002WO-US011359
                                                                                                                                                                           Homo sapiens.
                                                                                                                24-OCT-2002.
                                                                                                                                             WO200283068-A2.
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33.3%;
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Morrison K, Morrison RK, Ge
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Pred. No. 2e+06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH; humoral immune response; cellular immune response; suppression subtractive hybridisation; HLA; human leukocyte
            Challita-Eid PM, Rait
Afar DEH, Saffran D,
                                                                                                                                                             10-APR-2001; 2001US-0282739P.
25-APR-2001; 2001US-0286630P.
22-JUN-2001; 2001US-0300373P.
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Afar DEH, Saffran D, Morrison
                                                                                                       (AGEN-) AGENSYS INC.
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The invention relates to a novel composition comprising a substance that CC modulates the status of a protein, 121P2A3. The composition of the CC invention has cytostatic and immunostimulant activity, and is useful as a CC vaccine. The 121P2A3 proteins and polynucleotides are useful for CC eliciting humoral or cellular immune response. The polynucleotides are CC useful for characterising cytogenetic abnormalities of this chromosomal CC locus, as tools that can be used to delineate cytogenetic abnormalities CC in the chromosomal region that encodes 121P2A3 that may contribute to CC malignant phenotype, and in assessing the status of 121P2A3 gene products CC in normal versus cancerous tissues. The proteins are useful for CC generating and characterising domain-specific antibodies, for identifying agents or cellular factors that bind to 121P2A3 or a particular structure CC domain, and in various therapeutic and diagnostic contexts, including CC cancer vaccines. The antibodies or T cells reactive with the product are CC useful in passive or active immunisation, and in imaging methodologies CC represent peptides from the 121P2A3 variants of the invention
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Search completed: November 29, Job time: 96.4546 secs 밁 Ś Query Match Best Local S Matches 2 Similarity 2; Conserv N 4 YXXXXL YSTTTL Conservative 57.9%; 2005, 22:52:19 0; Score 11; DB Pred. No. 2e+0 0; Mismatches 2e+06; DB 6; 4. Length 9; Indels 0, Gaps

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RESULT 2 D82306 hypothetical protein VC0584 [imported] - Vibrio cholerae (strain N16961 c)Species: Vibrio cholerae C;Species: Vibrio cholerae C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2 C;Accession: D82306 R;Heidelberg, J.F; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi 1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000 A;Title: DNA Sequence of both chromosomes of the cholera pathogen vibrio A;Reference number: A82035; MUID:20406833; PMID:10952301 A;Accession: D82306 A;Status: preliminary A;Rosidues: 1-38 <hei>A;Cross-references: UNIPROT:09KUD8; UNIPARC:UPI00000C2D29; GB:AE004143; A;Genetics:</hei>	Query Match 57.9%; Score 11; DB 2; Length 15; Best Local Similarity 33.3%; Pred. No. 89; Matches 2; Conservative 0; Mismatches 4; Indels 0;  Qy 4 YXXXXL 9 1   1   Db 2 YSSSSL 7	an (fragment) 1993 #text_change , B.A.; Shane, S.; g in young childre D:1460419	30 11 57.9 94 2 A01955 Ig kappa -Bi 31 11 57.9 95 2 S45324 Ig kappa cl 32 11 57.9 95 2 S69898 Ig kappa cl 33 11 57.9 95 2 PH0863 Ig kappa cl 34 11 57.9 98 2 PH0863 Ig kappa cl 35 11 57.9 101 2 S44117 Ig kappa cl 36 11 57.9 101 2 C28840 Ig kappa cl 37 11 57.9 101 2 E328840 Ig kappa cl 38 11 57.9 101 2 B37262 Ig kappa cl 39 11 57.9 102 2 B37262 Ig kappa cl 40 11 57.9 104 2 F87731 Ig kappa cl 41 11 57.9 105 2 S36266 Ig kappa cl 42 11 57.9 106 2 PL0259 Ig kappa cl 43 11 57.9 106 2 PL0262 Ig kappa cl 44 11 57.9 106 2 PL0262 Ig kappa cl 45 11 57.9 107 2 S36264 Ig lambda cl 46 11 57.9 107 2 S36264 Ig lambda cl 47 11 57.9 107 2 S36266 Ig kappa cl 48 11 57.9 107 2 S36266 Ig kappa cl 49 11 57.9 107 2 S36266 Ig kappa cl 40 11 57.9 107 2 S36266 Ig lambda cl 41 11 57.9 107 2 S36266 Ig lambda cl 42 11 57.9 107 2 S36266 Ig lambda cl 43 11 57.9 107 2 S36266 Ig lambda cl 44 11 57.9 107 2 S36266 Ig lambda cl 45 11 57.9 107 2 S36266 Ig lambda cl
N16961 serogroup O1) )9-Jul-2004 nn, M.L.; Dodson, R.J. Dragoi, I.; Sellers. 1 Vibrio cholerae. 104143; GB:AE003852; Nor	); Gaps 0;	07-May-1999 Rovera, G. n with B precursor	o o o o z = 0 z = 0
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A;Molecule type: DNA
A;Residues: 1-46 <STO>
A;Cross-references: UNIP
A;Experimental source: 8
A;Accession: B85717
  14K hypothetical thioredoxin-related cycX 3'C;Species: Bradyrhizobium japonicum C;Date: 30-Dec-1991 #sequence_revision 30-Dec
                                                                      RESULT 5
E39741
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A;Note: the sequence shown here is one of eight productive V-D-J
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;1-49/Domain: V region <VRE>
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A; Residues: 1-54 < ANK>
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J. Exp. Med. 169, 2109-2119, 1989

A;Title: Clonal diversity in the B cell repertoire of patients with X-linked agammaglobu
A;Reference number: JT0511; MUID:89279157; PMID:2786547
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A;Experimental source: strain O157:H7, substrain EDL933
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A;Accession: E85743
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A;Reference number: A85480; MUID:21074935; PMID:11206551
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;Date: 23-Oct-1992 #sequence_revision 23-Oct-1992 #text_change 09-May-1997
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robium japonicum
#sequence_revision 30-Dec-1991 #text_change 09-Jul-2004
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Pred. No. 2e+0
0; Mismatches
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                                                                                                                                                                                                                                               Score 11; DB 2;
Pred. No. 2.3e+02;
0; Mismatches 4
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2e+02;
                                             region protein -
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                                               Bradyrhizobium japonicum
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                      A;Reference number: A99629;
A;Accession: F90970
A;Status: preliminary
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C;Accession: F90970
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, A.; Arayama, R;Hayashi, T.; Makino, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA, Res. 8, 11-22, 2001
DNA, Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: 3
C;Superfamil:
C;Keywords:
                                                                                                                                       probable head completion protein [imported] - Escherichia coli (
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change
C;Accession: F90970
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R;Ramseler, T.M.; Winteler, H.V.; Hennecke, H.
J. Biol. Chem. 266, 7793-7803, 1991
A;Title: Discovery and sequence analysis of bacterial genes involved in A;Reference number: A39741; MUID:91210304; PMID:1850420
A;Accession: E39741
A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-61 <ARM>
A;Residues: 1-64 <ARM>
A;Cross-references: UNIPROT:P30959; UNIPARC:UPI000005E784; GB:M60874; NI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPARC:UPI0000174BC3
A;Note: sequence extracted from NCBI backbone (NCBIN:129221, NCBIP:129224)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Smith, M.P.; Feiss, M.
J. Bacteriol. 175, 2393-2399, 1993
A;Title: Sites and gene products involved in lambdoid phage DNA
A;Title: number: A49849; MUID:93224462; PMID:8468297
A;Accession: C49849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene 126, 1-7, 1993
A;Title: Sequence analysis of the phage 21
A;Reference number: JN0537; MUID:93231520;
A;Accession: JN0537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-27 <SM2>
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A;Residues: 1-68 <SMI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Date: 17-Feb-1994 #sequence_revision;Accession: JN0537; C49849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Superfamily: phage lambda head-to-tail joining protein Keywords: head protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;Species: phage
;Date: 17-Feb-19
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Best Local
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Pred. No. 2.7e+02;
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2.5e+02;
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                                                      genon
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C;Species: vaccinia virus
A;Note: host Homo sapiens (man)
C;Date: 09-Nov-1990 #sequence_revision 09
C;Accession: F42516
R;Johnson, G.P.
submitted to GenBank, June 1990
A;Reference number: A33172
A;Accession: F42516
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A;Cross-references: UNIPROT:Q8XC12; UNIPARC:UPI0000D0524; GB:BA000007; PIDN:BAB36157.1
A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: A03878
R;NIles, E.G.; Condit, R.C.; Caro, P.; Davidson, K.; Matusick, L.; Seto, J.
Virology 153, 96-112, 1986
A;Title: Nucleotide sequence and genetic map of the 16-kb vaccinia virus HindIII D fragm
A;Reference number: A01146; MUID:86291159; PMID:3739227
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         Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 25-Oct-1996 #text_change 23-Jul-1999
C;Accession: S34082; S21526
                                                                                   RESULT 10
S21526
                                                                                                                                                                                                                                                                                                   A/Cross-references: UNIPROT:P20552; UNIPARC:UPI000013C1D1 C/Superfamily: vaccinia virus D-ORF-C protein
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A;Molecule type: DNA
A;Residues: 1-69 <JOH>
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C;Superfamily: vaccinia virus D-ORF-C protein
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A; Residues: 1-69 <NIL>
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C;Species: vaccinia virus
C;Date: 04-Dec:1986 #sequence_revision 04-Dec-1986 #text_change 09-Jul-2004
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Similarity 33.3%;
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Pred. No. 2.8e+02;
0; Mismatches 4
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Pred. No. 2.7e+02;
0; Mismatches 4
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Pred. No. 2.8e+0
0; Mismatches
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A,Cross-references: UNIPARC:UPI000011604F; EMBL:X66042; NID:g33318; C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
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A;Molecule type: DNA
A;Residues: 1-71 <WA2>
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A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributë
A;Reference number: S34076; MUID:93170387; PMID:8436174
A;Accession: S34082
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C89872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein a183L - Chlorella virus PBCV-1
C;Species: Chlorella virus PBCV-1
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Graves, M.V.; Van Etten, J.L. submitted to the EMBL Data Library,
                                                                                                                                                                                                                                      C;Accession: C89872
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; ma, A.; Misutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
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A; Residues: 1-76 < GRA>
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A; Accession: T17673
                                                                                                                                                    A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-81 <KUR>
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                                                                                                                     A; Experimental source:
                                                                                                                                                                                                                     A; Accession: C89872
Query Match
Best Local S
Matches 2
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Experimental source: strain N315
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33.3%;
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Pred. No. 3e+02;
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                       Score 11; I
Pred. No. 3.
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RESULT 15
316840
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S16840
R;Blaison, G.; Kuntz, J.L.; Pasquali, J.L.
Bur. J. Immuncol. 21, 1221-1227, 1991
A;Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fact A;Reference number: S16823; MUID:91243737; PMID:1903706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Wagner, S.D.; Luzzatto, L. Eur. J. Immunol. 23, 391-397, 1993
Eur. J. Immunol. 23, 391-397, 1993
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distribute
A;Reference number: S34076; MUID:93170387; PMID:8436174
A;Accession: S34086
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C;Species: Homo mapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
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A;Molecule type: DNA
A;Residues: 1-84 <STO>
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A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: F87306
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A; Residues: 1-86 < WAG>
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C;Superfamily: conserved hypothetical protein HI1000
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leb 2; Conservation
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Pred. No. 3.2e+02;
0; Mismatches 4
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Pred. No. 3.2e+02;
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A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-86 <ABLA>
A;Residues: 1-86 <ABLA>
A;Cross-references: UNIPROT:Q96SA9; UNIPARC:UPI0000176DA5; EMBL:X54838
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
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Search completed: November 29, Job time : 17.6818 secs
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Perfect score:
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      protein search,
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Copyright (c) 1993 - 2005
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Q65KLB BACOL
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Q87WA9_RHIET
Q57FQ4_9VIRU
Q5GAB8_9VIRU
Q6GAU3_FRGJV
Q6GZU3_FRGJV
Q67KG6_GRYSA
Q7UDB0_SHIFL
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Q5UM11_FRAAN
Q4YLV5_PLABE
Q9KUD8_V1BCH
Q8XC12_BCO57
Q6CVL2_KLULA
Q9AFM3_SHIFL
Q9AMSI BRAJA
Q7MRV7_WOLSU
Q775T4_CAMPS
Q67W10_ORYSA
Q6CB16_YARLI
Q6G147_PIPJA
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Q7ACV9_ECO57
Q5PAU6_ANAMM
Q8FIH6_ECOL6
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73.562 Million cell updates/sec
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Compugen Ltd.
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Q5pau6
Q8fih6
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Q6cv12
Q9afm3
Q57gg2
Q6x818
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Q6bxj7
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01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
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01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Glycosyltransferase family protein 47 (Fragment).
Fragaria ananassa (Strawberry).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Rosales; Rosaceae; Rosoideae; Fragaria.
NCBI TaxID=3747;
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EMBL; AY679583; AAV33443.1; -; mRNA,
GO; GO:0016740; F:transferase activi
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Balogh A., Koncz T., Kiss
"Identification of novel
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             3645 MW;
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Result

EMBL/GenBank/DDBJ databases

activity;

Heszky L.E.; s involved in ripening of strawberry

FFA703CB4A5C8A39 CRC64;

Minimum Maximum

Searched:

Database

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## Hypothetical protein. Schistosoma japonicum (Blood fluke). Sukaryota; Metazoa; Platyhelminthes; Schistosomatoidea; Schistosomatidae; Submitted (MAR-2005) to the EMBL; AY811905; AAX27794.1; Hypothetical protein. SEQUENCE 23 AA; 2622 MW; 57.9**%**; 33.3**%**; Last Last EMBL/GenBank/DDBJ -; mRNA. Created) Score 11; DB 2; Pred. No. 1e+03; 0; Mismatches 473EC523C9AF9967 PRT; sequence update) annotation update) Trematoda; Digenea; Strigeidida; Schistosoma. 23 DB 2; update) Å CRC64; databases Length 23; Indels 0 Gaps 0

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STRAIN=El Tor N16961 / Serotype O1;

STRAIN=El Tor N16961 / Serotype O1;

MEDLINE=20406833; PubMed=10952301; DOI=10.1038/35020000;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwir

Dodson R.J., Haft D.H., Hickey B.K., Peterson J.D., Umayam |

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson

Ermolaeva M.D., Vamathevan J.J., Bass S., Qin H., Dragoi I.

Ermolaeva M.D., Vamathevan J.J., Bass S., Qin H., Dragoi I.

McDonald L.A., Utterback T.R., Fleischmann R.D.
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01-OCT-2000
01-JUN-2003
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13-SEP-2005
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                                                                                                                                                                                                                                                     Vibrio cholerae.
Bacteria; Proteobacteria;
Vibrionaceae; Vibrio.
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Eukaryota; Alveolata; Apicomplexa;
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CAAI01003773; CAI01006.1;
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MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
"Genome semmence of ----
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Q8XC12_F
Q8XC12;
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13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Putative head completion protein of prophage CP-9330
packaging protein of prophage CP-933R).
OrderedLocusNames=z2132, z2363;
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP;
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PIR; F90970; F90970.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature
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GO:0019067; P:viral
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PF02831; gpW; 1.
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(TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
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J.C., Fraser C.
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Pred. No. 1.8e+03;
D; Mismatches 4
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MEDLINE=21189246; PubMed=11292750;
DOI=10.1128/IAI.69.5.3271-3285.2001;
Venkatesan M.M., Goldberg M.B., Rose D.J.,
Blattner F.R.;
"Complete DNA sequence and analysis of the shidella flexneri.";
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                                                                                                                                                                                       Infect. Immun. 69:3271-3285(2001).
EMBL, AF348706; AAK18846.1; -; Gen
Hypothetical protein; Plasmid.
BEQUENCE 49 AA; 5174 MW; 81FEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmid virulence plasmid pWR501.
Bacteria, Proteobacteria, Gammaproteobacteria,
Enterobacteriaceae, Shigella.
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Q9AFM3;
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EMBL; CR382122; CAH02420.1; -;
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"The mitochondrial genome of the olive fly Bactrocera oleae: two rappolitypes from distant geographical locations.";

RI Insect Wol. Biol. 12:605-611(2003).

RMBL; AY210703; AA034658.1; -; Genomic_DNA.

RMBL; AY210702; AA034658.1; -; Genomic_DNA.

RGO; GO:0016020; C:nembrane; IEA.

DR GO; GO:0016020; C:nembrane; IEA.

DR GO; GO:0045263; C:proton-transporting ATP synthase complex; C:.; 1 GO; GO:0016469; C:proton-transporting two-sector ATPase complex; IEA.

DR GO; GO:0046933; F:hydrogen-transporting ATP synthase activity...; I GO; GO:0015986; P:hydrogen-transporting ATPase activity...; I GO; GO:0015986; P:hydrogen-transporting ATPase activity. rota...; I GO; GO:0015986; P:hydrogen-transporting ATPase activity. rota...; I GO; GO:0015986; P:hydrogen-transport; IEA.

DR GO; GO:0015986; P:hydrogen-transport; IEA.

DR GO; GO:0015986; P:hydrogen-transport; IEA.

DR GO; GO:001421; ATPase88 mit.

DR InterPro; IPR001421; ATPase88 mit.

DR Hydrogen ion transport; Ion transport; Mitochondrion: KW CF(0); Hydrogen ion transport; Ion transport; Mitochondrion: Transport; Transport; Transport; Transport; Transport; Mitochondrion: Transport; Transport; Transport; Mitochondrion: Transport; Transport; Transport; Mitochondrion: Transport; Transport; Mitochondrion: Transport; Transport; Mitochondrion: Transport; Transport; Mitochondrion: Transport; Transport; Mitochondrion: Transport; Transport; Mitochondrion: Transport; Transport; Mitochondrion: Transport; Transport; Mitochondrion: Transport; Transport; Mitochondrion: Transport; Mitochondrion: Transport; Transport; Mitochondrion: Transport; Transport; Mitochondrion: Transport; Mitochondrion: Transport; Mitochondrion: Transport; Mitochondrion: Transport; Mitochondrion: Transport; Mitochondrion: Transport; Mitochondrion: Transport; Mitochondrion: Transport; Mitochondrion: Transport; Mitochondrion: Transport; Mitochondrion: Transport; Mitochondrion: Transport; Mitochondrion: Transport; Mitochondrion: Transport; Mitochondrion: Transport; Mitochondrion: Transport; Mitochondrion: Transpo
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10-MAY-2005 (TrEMBLrel. 30, Last sequence upda ATP synthase F0 subunit 8.
Bactrocera oleae (Olive fruit flooring)
Mitochondrion.
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EMBL; AE017220; AAX68200.1; -; Genomic_DNA.
Complete proteome; Hypothetical protein.
SEQUENCE 51 AA; 5645 MW; BF41842EEDF831DB CRC64;
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
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OrderedLocusNames=SC4294;
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Tephritoidea; Tephritidae; Bactrocera; Daculus.
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RESULT 10
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01-JUL-1993 (
01-JUL-1993 (
10-MAY-2005 (
                                                                                                       TRANSMEM
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                 EMBL; M60874; AAA26195.1; -; Genomic_DNA.
EMBL; BA000040; BAC45735.1; -; Genomic_DN
PIR; E39741; E39741.
                                                                                                                                                                                                                                                             This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
                                                                                                                                                                                                                                                                                                                                                        "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110."; DNA Res. 9:189-197(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ramseier T.M., Winteler H.V., Hennecke H.;
"Discovery and sequence analysis of bacterial genes biogenesis of c-type cytochromes.";
J. Biol. Chem. 266:7793-7803(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bradyrhizobium japonicum.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobialea;
Bradyrhizobiaceae; Bradyrhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BRAJA
                                                                                                                                                                                                                                                                                                                                                                                                          Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashin
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
10-MAY-2005 (Rel. 47, Last annotation update)
Heme exporter protein D (Cytochrome c-type biggenesis protein
Name=cycX; Synonyms=ccmD; OrderedLocusNames=bsr0470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCMD
                                                                                                                  Complete proteome; Cytochrome c-type biogenesis;
Membrane; Transmembrane; Transport.
TRANSMEM 11 31 Potential.
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                                                                                                                                                        Pfam; PF04995; CcmD;
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                                                                                                                                                                                                                                                      use as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22484998; PubMed=12597275;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=375;
                                                                                                                                                                                                                                                                                                             Res. 9:189-197(2002).

FUNCTION: Required for the export of heme to the biogenesis of c-type cytochromes (Potential).

SIMILARITY: Belongs to the ccmD/cycX/helD family.
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16
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YAAAAL 21
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                                                                                                     61 AA; 6776 MW;
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                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49
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33.3%;
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                                                 Score 11; DB Pred. No. 2.3e 0; Mismatches
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Pred. No.
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BC6B9852E927370A CRC64;
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                                                                                                                                             Inner membrane;
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RESULT 11

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Q6BXJ7_DEBHA
ID Q6BXJ7;
AC Q6BXJ7;
AC Q6BXJ7;
AC Q6BXJ7;
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QBVMA9 RHIET
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Matches 2
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A Lafontaine I. de Montigny J., Marck C., Neuveglise C., Talla E.,
A Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
A Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
A Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Darnvar A.,
A Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
A Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
A Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
A Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
A Kerrest A., Nicolaki M., Oztas S., Ozier-Kalogeropoulos O.,
A Pellenz S., Potter S., Richard G.-F., Straub M.-L., Suleau A.,
A Swennen D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
A Seniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
Mincker P., Souciet J.-L.;
Query Match
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OBVMAP 2002 (TrEMBLrel. 2
01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                         NON_TER
                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
NCBI_TaxID=29449;
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                                                 SEQUENCE
                                                                                                                        development phenotypes.";
Mol. Plant Microbe Interact.
EMBL; AJ422134; CAD19513.1;
                                                                                                                                                                                                                                                                                                       STRAIN=CE3
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhizobium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=lysA;
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Debaryomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OrderedLocusNames=DEHA0B02453g;
                                                                                                                                                                                                                                                                          MEDLINE=22031767; PubMed=12036281;
                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE
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EMBL; CR382134; CAG85060.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                        Ferraioli
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  57.9%;
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                                                                                                                                               15:501-510(2002)
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Pred. No. 2.3e+0
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                                                 B94868D845DAAE9A CRC64;
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Pred. No. 2.3e+03; 0; Mismatches 4;

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Chang C.-Y., Tsai C.-Y.
"The complete genome a submitted (FEB-2005)
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10-MAY-2005
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PubMed=15681403; DOII10.1128/JVI.79.4.2010-2023.2005;

Pasi C.T., Ting J.W., Wu M.H., Wu M.F., Guo I.C., Chang (
"Complete genome sequence of the grouper iridovirus and (
genomic organization with those of other iridoviruses.";

J. Virol. 79:2010-2023(2005).
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Song W.J., Oln Q.W., Qlu J., Huang C.H., Wang F., Hew C.L.;

Song W.J., Oln Q.W., Qlu J., Huang C.H., Wang F., Hew C.L.;

"Functional Genomics Analysis of Singapore Grouper Iridovirus:

Complete Sequence Determination and Proteomic Analysis.";

J. Virol. 78:12576-12590 (2004).

EMBL; AV521625; AAS18026.1; -; Genomic_DNA.

Hypothetical protein.

Hypothetical protein.

SEQUENCE 62 AA; 6634 MW; C7B664F54B70AC86 CRC64;
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A 9VIRU PRELIMINARY;
OSYFO4 9VIRU PRELIMINARY;
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25-OCT-2004 (TrEMBLrel.
Hypothetical protein.
ORFNames=ORF011L;
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Viruses; dsDNA viruses,
NCBI_TaxID=127569;
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Viruses, dsDNA viruses, no RNA
                           NUCLEOTIDE SEQUENCE.
Chang C.-Y., T8ai C.-T.;
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Submitted (JUN-2004) to the
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Murali S., Wu M.-F.,
Submitted (MAR-2001)
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Q6GZU3;
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05-JUL-2004 (TrEMBLrel. 2
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Tan W.G.H., Barkman T.J., Chinchar V.G., Essani
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ da
EMBL; AY548464; AAT09692.1; -; Genomic_DNA.
Hypothetical protein.
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PubMed=15165820; DOI-10.1016/j.virol.2004.02.019;
Pan M.G., Barkman T.J., Gregory Chinchar V., Essani
"Comparative genomic analyses of frog virus 3, type
genus Ranavirus (family Iridoviridae).";
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                                                                                                                                                                                                                                                                                              Hypothetical protein. Frog virus 3 (FV3).
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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length: 2000000000
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    Issued_Patents_AA:*

1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/AE_COMB.pep:*
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US-09-63-600A-22
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US-09-835-832A-37
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Query Match 57.9%; Best Local Similarity 33.3%; Matches 2; Conservative

0;

Score 11; DB 1; Pred. No. 1.4e+03; Mismatches

Length 11;

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RESULT 3
US-09-051-342-123
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US-08-540-412-191
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                                                                          Patent No. 6130204
GENERAL INFORMATION:
APPLICANT: DeFeo-Jones, Deborah
APPLICANT: Feng, Dong-Mei
APPLICANT: Garsky, Victor M.
APPLICANT: Jones, Raymond E.
                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 2; Conservat
                                                                                                                                                                             Sequence 123, Application US/09051342
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APPLICANT: Defeo-
APPLICANT: Feng, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (908)594-4720
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                 CORRESPONDENCE ADDRESS:
                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 19:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Muthard, David A.
REGISTRATION NUMBER: 35,
                              TITLE OF INVENTION: NOVEL PEPTIDES NUMBER OF SEQUENCES: 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Garsky, Victor M. APPLICANT: Jones, Raymond E. APPLICANT: Oliff, Allen I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acids
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ADDRESSEE:
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TOPOLOGY: linear
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                                                           Garsky, Victor M.
Jones, Raymond E.
Oliff, Allen I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 E. Lincoln Avenue, P.O. BOX 2000
                                                                                                                                                                                                                                                                                                                              Conservative
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 DAVID A. MUTHARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (908) 594-3903
                                                                                                                                                                                                                                                                                                                                                                                                         peptide
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33.3%;
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Pred. No. 1.4e+03;
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; HYPOTHETICAL: NO; ANTI-SENSE: NO; FRAGMENT TYPE: : US-09-051-342-123
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US-09-051-342-191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 191, Application US/09051342 Patent No. 6130204
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Best Local Similarity 33.3%;
Matches 2; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
ANAME: Muthard, David A.
REGISTRATION NUMBER: 35,297
REFERENCE/DOCKET NUMBER: 1925
TELECOMMUNICATION INFORMATION:
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Muthard, David A.
REGISTRATION NUMBER: 35,;
                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/051,342
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/051,342
                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: NOVEL PEPTIDES NUMBER OF SEQUENCES: 194
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                                                                                                                                                                                                                    STATE: NEW JERSEY COUNTRY: U.S.A. ZIP: 07065
                                                                                                                                                                                                                                                                              CITY: RAHWAY
                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                              ADDRESSEE: DAVID A. MUTHARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                 T: DeFeo-Jones, Deborah
T: Feng, Dong-Mei
T: Garsky, Victor M.
T: Jones, Raymond E.
T: Oliff, Allen I.
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                                                                                                                                                                                                                                                                                           126 E. Lincoln Avenue, P.O. BOX 2000
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Pred. No. 1.4e
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Query Match
Best Local Similarity
"---hes 2; Conserve
                                                                                US-08-468-161-123
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Best Local Similarity 33.3%;
Matches 2; Conservative
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Patent No. 6143864
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SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                        CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: MUTHARD DAVID A: 35,297
REGISTRATION UNMBER: 1925
REFERENCE/DOCKET NUMBER: 1925
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-3903
                                                                                                                                                                                                                          TELEFAX: (908)594-4720
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                             MOLECULE TYPE: |
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-3903
                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                     LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Oliff Allen I.
TITLE OF INVENTION: NOVEL PEPTIDES
NUMBER OF SEQUENCES: 146
CORRESPONDENCE ADDRESS:
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COUNTRY: U.S.A.
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STRANDEDNESS: sir
TOPOLOGY: linear
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Jones, Raymond E.
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               Conservative
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                                                                                                 internal
                                                                                                                                             peptide
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                              57.9%;
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Pred. No. 1.4e+03;
0; Mismatches 4
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               Score 11; DB 2; 1 Pred. No. 1.4e+03; 0; Mismatches 4
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                                              Length 11;
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FEATURE:
OTHER INFORMATION: completely synthetic amino acid sequence
US-09-051-759-123
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US-09-051-759-123
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; OTHER INFORMATION; completely synthetic amino acid sequence US-09-051-759-191
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SEQ ID NO 123
LENGTH: 11
                                                                             SOFTWARE: FA
SEQ ID NO 191
LENGTH: 11
TYPE: PRT
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Matches 2; Conservative
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TITLE OF INVENTION: CONJUGATES USEFUL IN THE TREATMENT OF
TITLE OF INVENTION: BENIGN PROSTATIC HYPERPLASIA
FILE REFERENCE: 19560P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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CURRENT FILING DATE: 1998-08-03
PRIOR APPLICATION NUMBER: 60/005,664
PRIOR FILING DATE: 1995-10-18
PRIOR APPLICATION NUMBER: PCT/US96/16490
PRIOR FILING DATE: 1996-10-15
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APPLICANT:
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APPLICANT:
                                                                                                                                                                                                                                                                                                APPLICANT: Garsky, Victor M.
APPLICANT: Jones, Raymond E.
APPLICANT: Oliff, Allen I.
APPLICANT: Scolnick, Edward M.
TITLE OF INVENTION: CONJUGATES USEFUL IN THE TREATMENT
TITLE OF INVENTION: BENIGN PROSTATIC HYPERPLASIA
FILE REFERENCE: 19560P
                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/051,759
CURRENT FILING DATE: 1998-08-03
PRIOR APPLICATION NUMBER: 60/005,664
PRIOR FILING DATE: 1995-10-18
PRIOR APPLICATION NUMBER: PCT/US96/16490
PRIOR FILING DATE: 1996-10-15
PRIOR FILING DATE: 1996-10-15
PRIOR FILING DATE: 1996-10-15
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                                       ORGANISM: Artificial Sequence FEATURE:
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DeFeo-Jones, Debor
Garsky, Victor M.
Jones, Raymond E.
Oliff, Allen I.
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                                                                                                                                          FastSEQ for Windows Version 4.0
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Pred. No. 1.4e
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Query Match
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Best Local Similarity
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                                      RESULT 9
5219837-5
;Patent No. 5219837
; APPLICANT: COHEN, JEFFREY A.;GREENE, MARK I.;WILLIAMS,
;WILLIAM V.
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PCT-US95-08156-123
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              OF CELLS
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                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (908)594-4720 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                 HYPOTHETICAL: N
ANTI-SENSE: NO
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
TOPOLOGY: ling
MOLECULE TYPE:
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Muthard, David A.
REGISTRATION NUMBER: 35,297
REFERENCE/DOCKET NUMBER: 19;
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                          TITLE OF INVENTION: METHOD OF STIMULATING MYELINATION
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID A. MUTHARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US95/08156 FILING DATE: CLASSIFICATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U
ZIP: 07065
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amino acid
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Jones, Raymond E.
Oliff, Allen I.
                                                                                                                                                                                               Conservative
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Pred. No. 1.4e+03;
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Pred. No. 1.4e+03;
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APPLICATION NUMBER: US/07/541,779
FILING DATE: 21-JUN-1990
;SEQ ID NO:5:
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                       US-08-905-223-22
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Best Local Similarity 33...
Conservative
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Best Local Similarity 33...
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Harris, Curtis C
APPLICANT: Nagashima, Makoto
APPLICANT: Nagashima of United States as represented by the Secretary of the APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: New Tumor Suppressor Gene P33ING2
FILE REFERENCE: 015280-376100US
                                                                                                                                                                                                                                                                                  Sequence 22, Applicat Patent No. 6222029
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/09513365A Patent No. 6790948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/121,891
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/513,365A CURRENT FILING DATE: 2000-02-25
ZIP: 92101-3505
COMPUTER READABLE FORM:
COMPUTER: Floppy Disk
COMPUTER: IBM PC Compatib:
OPERATING SYSTEM: Win95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: peptide 7-26 OTHER INFORMATION: of p33ING2 (KMP1)
                                                                                                                                                                              APPLICANT: Edwards, Jean-Baptiste w. APPLICANT: Duelert, Aymeric APPLICANT: Lacroix, Bruno TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS NUMBER OF SEQUENCES: 503
                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                         STREET: 501 West
                                                                                         COUNTRY: USA
                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 YSASTL 17
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                                                                                                           California
                                                                                                                                        E: Knobbe, Martens, Olson & Bear
501 West Broadway
                                                                                                                                                                                                                                                                                                                       Application US/08905223
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Pred. No. 2.1e+03;
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Pred. No. 1.9e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 20
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Sequence 22, Application US/09247155A

Patent No. 6312922

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Duclert, Aymeric
APPLICANT: Bouqueleret, Lydie
TITLE OF INVENTION: Complementary DNAs
FILE REFERENCE: GENSET.021A
CURRENT FILING DATE: 1999-02-09
EARLIER APPLICATION NUMBER: 60/074,121
EARLIER FILING DATE: 1998-02-09
EARLIER FILING DATE: 1998-02-09
EARLIER FILING DATE: 1998-04-13
EARLIER FILING DATE: 1998-04-13
EARLIER FILING DATE: 1998-08-10

EARLIER APPLICATION NUMBER: 60/096,116
EARLIER APPLICATION NUMBER: 60/096,116
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                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 182
SOFTWARE: Patent.pm
SEQ ID NO 22
LENGTH: 37
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Matches 2; Conserv
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Query Match 57.9%; Score 11; DB 2; Best Local Similarity 33.3%; Pred. No. 3.1e+03; Matches 2; Conservative 0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acide
TYPE: AMINO ACID
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                EARLIER APPLICATION NUMBER: 60/099,273
EARLIER FILING DATE: 1998-10-04
                                                                                                      LOCATION: 1..37
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 5.9
OTHER INFORMATION: seq LSYASSALSPCLT/AP
                                                                                                                                                                                           FEATURE:
NAME/KEY: SIGNAL
                                                                                                                                                                                                                                     ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
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APPLICATION NUMBER: US/08/905,223
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 1.37
IDENTIFICATION METHOD: Von Heijne matrix
OTHER INFORMATION: score 5.9
OTHER INFORMATION: seq LSYASSALSPCLT/AP
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LOCATION: 1..37
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US-09-903-190-22
; Sequence 22, Application US/09903190
; Patent No. 6936592
; GENERAL INFORMATION:
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LENGTH: 37
                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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         APPLICANT: Dumás Milne Edwards, Jean-Baptiste
APPLICANT: Duclert, Aymeric
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: Complementary DNAs
FILLE REPERENCE: GENSET.021A
CURRENT APPLICATION NUMBER: US/09/903,190
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: US/09/247,155A
PRIOR FILING DATE: 1999-02-09
PRIOR FILING DATE: EARLIER APPLICATION NUMBER: 60/074,121
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/081,563
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/081,563
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:

NAME/KEY: SIGNAL

LOCATION: 1..37

OTHER INFORMATION: V

OTHER INFORMATION: S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS FILE REFERENCE: 31.US3.CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity nes 2; Conserv
FILING DATE: EARLIER FILING DATE: 1998-04-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq LSYASSALSPCLT/AP
                                                                                                                                                                                                                                                                                                                                                                                                  57.9%;
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Pred. No. 3.1e+03;
0; Mismatches 4
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PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/096,116
PRIOR FILING DATE: EARLIER FILING DATE: 198-08-10
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/099,273
PRIOR FILING DATE: EARLIER APPLICATION NUMBER: 60/099,273
VANDBER OF SEQ ID NOS: 182
SOFTWARE: Patent.pm
SEQ ID NO 22
LENGTH: 37
TYPE: PRT
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: 1..37
OTHER INFORMATION: SCORE 5.9
OTHER INFORMATION: SCORE 5.9
OTHER INFORMATION: SEQ LSYASSALSPCLT/AP
                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,586
FILING DATE: 07-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 02,678
REGISTRATION NUMBER: 0575/53862-A
TELECOMUNICATION: INFORMATION:
TELEPHONE: (212) 278-0400
TELEPAX: (212) 278-0400
TELEPAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acids
                                                                                 TOPOLOGY: linear; MOLECULE TYPE: protein US-08-812-586-40
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US-08-812-586-40
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Query Match 57.9%; Score 11; DB 2; Best Local Similarity 33.3%; Pred. No. 3.3e+03; Matches 2; Conservative 0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 40, Application US/08812586
Patent No. 6048704
GENERAL INFORMATION:
APPLICANT: Martin David Tilson
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        y Match 57.9%; Score 11; DB 2; Length 37; Local Similarity 33.3%; Pred. No. 3.1e+03; hes 2; Conservative 0; Mismatches 4; Indels
                                                                                                                                        LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
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PROTEINS ASSOCIATED WITH ABDOMINAL AORTIC ANEURYM (AAA)
DISEASE, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
                                        Length 40;
    4.
  Indels
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Search completed: November 29, 2005, 23:04:23 Job time: 24.8636 secs

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Minimum
Maximum
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No.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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19
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Match Length
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Maximum Match 100%
Listing first 45 summaries
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Published Applications AA Main:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
                      DB
                             US-10-105-545-8
US-11-073-349-65
US-11-073-349-65
US-10-105-545-21
US-10-109-643-54
US-10-109-945A-2
US-10-197-945A-2
US-10-197-945A-2
US-10-197-013-609
US-10-776-013-609
US-10-776-013-609
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US-10-10-815-67
US-10-10-815-67
US-10-10-815-67
US-10-10-815-67
US-10-10-115-261313
US-10-10-319-763-123
US-10-425-115-361971
US-10-276-774-2215
US-10-109-048-661
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           US-10-767-701-61017
US-10-424-599-208666
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           67, Appl
287301,
250421,
250421,
22, Appl
122, Appl
153132,
22, Appl
120714,
361971,
361971,
Appl
61017, Appl
61017, Appl
208666,
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65, Appl
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51, Appl
21, Appl
66, Appl
66, Appl
2, Appli
60, App
616, Appl
616, Appli
5, Appli
5, Appli
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US-10-105-545-8
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29 11 57 9 48 US-10-424-599-169349 30 11 57,9 49 US-10-425-115-20180 31 11 57,9 49 US-10-425-115-20180 32 11 57,9 49 US-10-425-115-321205 33 11 57,9 49 US-10-425-115-321305 34 11 57,9 50 US-10-425-115-321893 36 11 57,9 50 US-10-425-115-321893 37 11 57,9 50 US-10-425-135-32199 38 11 57,9 51 US-10-425-136935 39 11 57,9 52 US-10-424-599-17394 40 11 57,9 52 US-10-424-599-217394 41 11 57,9 53 US-10-424-599-171812 42 11 57,9 55 US-10-424-599-179378 43 11 57,9 55 US-10-424-599-179378 44 11 57,9 55 US-10-424-599-179378 45 11 57,9 55 US-10-424-599-179378 46 11 57,9 55 US-10-424-599-179378 47 11 57,9 55 US-10-424-599-179378 48 11 57,9 55 US-10-424-599-179378 49 11 57,9 55 US-10-424-599-179378	
57.9 49 4 57.9 50 4 6 6 6 57.9 5 57.0 5 57.0 5 57.0 5 57.0 5 57.0 5 57.0 5 57.0 5 57.0 5 57.0 5 57.0 5 57.0 5 57.0 5 57.0 5 57.0 5 57.0 5 57.0 5 57.0 5 57.0 5 57.0	45
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US-10-424-599-169349 US-10-425-115-201880 US-10-425-115-321205 US-10-425-115-321205 US-10-425-115-32114 US-09-978-360A-624 US-10-425-115-321893 US-11-075-234-379 US-10-424-599-13194 US-10-424-599-171812 US-10-424-599-171812 US-10-424-599-171812 US-10-424-599-171812 US-10-424-599-171812 US-10-424-599-171812 US-10-424-599-171812 US-10-424-599-171812 US-10-424-599-171812 US-10-424-599-171812 US-10-424-599-171812 US-10-424-599-171812 US-10-424-599-171812 US-10-424-599-171812 US-10-424-599-171812	4
	US-10-425-115-317178

ALIGNMENTS

US.

CURRENT FILING DATE: 190-01-05

FILING MATE: 2002-09-06

PRIOR APPLICATION NUMBER: US 08/752,816

PRIOR APPLICATION NUMBER: US 07/940,654

PRIOR APPLICATION NUMBER: US 07/940,654

PRIOR PPLICATION NUMBER: US 07/940,654

PRIOR APPLICATION NUMBER: US 07/702,833

PRIOR FILING DATE: 1991-05-20

PRIOR APPLICATION NUMBER: US 07/326,328

PRIOR FILING DATE: 1991-05-20

PRIOR FILING DATE: 198-03-21

PRIOR PILING DATE: 198-07-16

PRIOR PILING DATE: 198-07-16

PRIOR APPLICATION NUMBER: US 07/642,542

PRIOR APPLICATION NUMBER: US 07/648,303

PRIOR APPLICATION NUMBER: US 07/648,303

PRIOR PILING DATE: 1991-01-05

PRIOR APPLICATION NUMBER: US 07/648,303

PRIOR APPLICATION NUMBER: US 07/648,303

PRIOR APPLICATION NUMBER: US 07/674,391

PRIOR APPLICATION NUMBER: US 07/574,391

PRIOR APPLICATION NUMBER: US 07/574,391

PRIOR APPLICATION NUMBER: US 07/574,391

PRIOR PILING DATE: 1990-08-27

PRIOR APPLICATION NUMBER: US 07/574,391

PRIOR APPLICATION NUMBER: US 07/574,391 US-10-105-545-8 Remaining Prior Application data NUMBER OF SEQ ID NOS: 32 SOFTWARE: PatentIn version 3.1 SEQ ID NO 8 LENGTH: 17 Query Match 57.9%; Best Local Similarity 33.3%; Matches 2; Conservative APPLICANT: Mark, Greene I.
APPLICANT: Williams, William V.
APPLICANT: Weiner, David B.
APPLICANT: Cohen, Jeffery A.
APPLICANT: Kieber-Emmons, Thomas APPLICANT: Williams, Robert M.
TITLE OF INVENTION: BIOLOGICALLY ACTIVE COMPOUNDS AND
TITLE OF INVENTION: SAME PRIOR APPLICATION NUMBER: US 07/194,026 PRIOR FILING DATE: 1988-05-13 FILE REFERENCE: 4040/1L492US2 OTHER INFORMATION: synthetic peptide FEATURE: ORGANISM: Artificial Sequence Score 11; DB 4; Lo Pred. No. 3.8e+03; 0; Mismatches 4; removed • See File Wrapper or PALM Length 17; METHODS ç CONSTRUCTING AND

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US-10-120-835-65
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SOFTWARE: FRSTSEQ for Windows Version 4.0
SEQ ID NO 65
LENGTH: 17
TYPE: PRT
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Publication No.
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Best Local (
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APPLICANT: Morrison, Karen J. M.
APPLICANT: Morrison, Robert K.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobovitz, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 12192A3 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20061.00
CURRENT APPLICATION NUMBER: US/11/073,349
CURRENT FILING DATE: 2005-03-03
                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: US 60/286,630
PRIOR FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: US 60/300,373
PRIOR APPLICATION NUMBER: US 60/300,373
PRIOR FILING DATE: 2001-06-22
NUMBER OF THE PRIOR FILING DATE: 2001-06-22
NUMBER OF THE PRIOR FILING DATE: 2001-06-22
NUMBER OF THE PRIOR FILING DATE: 2001-06-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Saffran, Douglas
APPLICANT: Morrison, Karen J. M.
APPLICANT: Morrison, Robert K.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobovitz, Aya
APPLICANT: Jakobovitz, Aya
APPLICANT: Jakobovitz, Aya
TITLE OF INVENTION: ENTITLED CACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 121P2A3 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20061.00
CURRENT APPLICATION NUMBER: US/10/120,835
CURRENT FILING DATE: 2002-09-12
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APPLICANT: Challita-Eid, Pia M.
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2; Conservative
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Mitchell, Steve C.
Afar, Daniel E. H.
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                                                                                                                                                 Saffran, Douglas
Morrison, Karen J. M.
Morrison, Robert K.
                                                                                                                                                                                                                  Hubert, Rene S.
Mitchell, Steve C.
Afar, Daniel E. H.
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Raitano, Arthur B.
Faris, Mary
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33.3%;
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Pred. No. 3.8e+03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 08/752,816
PRIOR FILING DATE: 1996-11-21
PRIOR APPLICATION NUMBER: US 07/940,654
PRIOR FILLING DATE: 1992-09-03
PRIOR APPLICATION NUMBER: US 07/702,833
PRIOR APPLICATION NUMBER: US 07/326,328
PRIOR FILLING DATE: 1991-05-20
PRIOR APPLICATION NUMBER: US 07/326,328
PRIOR FILLING DATE: 1989-03-21
PRIOR APPLICATION NUMBER: US 07/074,264
PRIOR FILLING DATE: 1987-07-16
                                                                                                                                                       Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1
SEQ ID NO 21
LENGTH: 18
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Matches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 65
LENGTH: 17
Query Match
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PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: US 60/286,630
PRIOR FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: US 60/300,373
PRIOR FILING DATE: 2001-06-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 4040/1L492US2
CURRENT APPLICATION NUMBER: US/10/105,545
CURRENT FILING DATE: 2002-09-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Williams, Willia APPLICANT: Weiner, David B.
                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 1990-01-09
PRIOR APPLICATION NUMBER: US 07/648,303
PRIOR FILING DATE: 1991-01-25
PRIOR APPLICATION NUMBER: US 07/685,881
PRIOR FILING DATE: 1991-04-15
PRIOR APPLICATION NUMBER: US 07/574,391
PRIOR FILING DATE: 1990-08-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Kieber-Emmons, Thomas
APPLICANT: Williams, Robert M.
TITLE OF INVENTION: BIOLOGICALLY ACTIVE COMPOUNDS AND METHODS OF CONSTRUCTING AND USING TITLE OF INVENTION: SAME
                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 07/194,026 PRIOR FILING DATE: 1988-05-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Mark,
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                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic peptide
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2; Conserv
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  57.9%; Score 11;
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Pred. No.

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    DB 4;
  Length 18;
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; Sequence 66, Application US/10120835
; Publication No. US20040018189A1
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                                                                                                                                             FILE REFERENCE: 51158-20061.00
CURRENT APPLICATION NUMBER: US/10/120,835
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: US 60/286,630
PRIOR APPLICATION NUMBER: US 60/300,373
PRIOR APPLICATION NUMBER: US 60/300,373
PRIOR APPLICATION NUMBER: US 60/300,373
PRIOR APPLICATION NUMBER: US 60/300,373
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APPLICANT: Hartzell, William
APPLICANT: Hartzell, William
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PREVENTING AND TREATING MICROBIAL I
TITLE REFERENCE: B00801.70281.US
CURRENT FILING NOMBER: US/10/409,643
CURRENT FILING DATE: 2003-04-08
PRIOR APPLICATION NUMBER: US 60/370,649
PRIOR APPLICATION NUMBER: US 60/370,649
PRIOR FILING DATE: 2002-04-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PATENTIN VETSION 3.1
SEQ ID NO 54
LENGTH: 18
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Best Local Similarity 33.3%;
Matches 2; Conservative
                                                            NUMBER OF SEQ ID NOS: 82
SOFTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 66
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
TYPE: PRT
ORGANISM: Homo Sapiens
-10-120-835-66
                                                                                                                                                                                                                                                                                                                                            APPLICANT: Jakobovitz, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 121P2A3 USEFUL IN TREATMENT !
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Hubert, Rene S.
Mitchell, Steve C.
Afar, Daniel E. H.
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Morrison, Karen J. M.
Morrison, Robert K.
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Pred. No. 4e+03;
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Sequence 66, Application US/11073349
Publication No. US20050214211A1
GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/11/073,349
CURRENT APPLICATION NUMBER: US/10/120,835
PRIOR APPLICATION NUMBER: US/10/120,835
PRIOR FILING DATE: 2002-09-12
PRIOR PPLICATION NUMBER: US 60/282,739
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: US 60/286,630
PRIOR APPLICATION NUMBER: US 60/286,630
PRIOR PILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: US 60/300,373
PRIOR PILING DATE: 2001-06-22
PRIOR FILING DATE: 2001-06-22
                                                                                                                                                                                                                                                                                                US-10-197-945A-2
                                                                                                                                                                                                                             Sequence 2, Application US/10197945A Publication No. US20040014148A1 GENERAL INFORMATION:
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SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 66
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Best Local
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APPLICANT:
APPLICANT:
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Best Local Similarity
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APPLICANT:
APPLICANT:
                                  APPLICANT: Masuda, Esteban
APPLICANT: Kinsella, Todd M
APPLICANT: Warner, Justin B
APPLICANT: Warner, Justin B
APPLICANT: Kinoshita, Taisei
APPLICANT: Kinoshita, Taisei
APPLICANT: Manett, Mark K
APPLICANT: Anderson, David C
TITLE OF INVENTION: Methods of Identifying Compounds that Modulate IL-4 Receptor-Med.
TITLE OF INVENTION: Synthesis Utlilizing a Chloride Intracellular Channel 1 Protein
FILE REFERENCE: RIGI-013/00US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 121P2A3 USEFUL IN TREATMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
CURRENT APPLICATION NUMBER: US/10/197,945A CURRENT FILING DATE: 2002-10-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 19
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Hubert, Rene S.
Mitchell, Steve C.
Afar, Daniel B. H.
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Morrison, Karen J. M.
Morrison, Robert K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Challita-Eid, Pia M. Raitano, Arthur B.
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33.3%;
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Pred. No. 4.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 11; DB 6;
Pred. No. 4.1e+03;
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RESULT 10
US-10-776-013-616
; Sequence 616, Application US/10776013
; Publication No. US20040226056A1
; GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 09/48904
PRIOR APPLICATION NUMBER: 09/48904
PRIOR APPLICATION NUMBER: 09/466139
PRIOR APPLICATION NUMBER: 09/466139
PRIOR APPLICATION NUMBER: 60/113534
PRIOR APPLICATION NUMBER: 60/113534
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/124120
PRIOR APPLICATION NUMBER: 60/124120
PRIOR APPLICATION NUMBER: 60/141243
PRIOR PILING DATE: 1999-03-12
PRIOR PILING DATE: 1999-06-30
PRIOR PILING DATE: 1999-06-30
PRIOR PILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240790
PRIOR PILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/240790
PRIOR PILING DATE: 2000-10-17
PRIOR PILING DATE: 2000-07-15
PRIOR APPLICATION NUMBER: 60/304775
PRIOR APPLICATION NUMBER: 60/304775
PRIOR APPLICATION NUMBER: 60/304775
PRIOR APPLICATION NUMBER: 60/304775
PRIOR APPLICATION NUMBER: 60/304775
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PRIOR APPLICATION NUMBER: 60/304775
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PRIOR APPLICATION NUMBER: 60/304775
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; ORGANISM: Homo sapiens
US-10-776-013-609
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US-10-776-013-609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 57.9
Best Local Similarity 33.3
Matches 2; Conservative
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LENGTH: 20
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 609
LENGTH: 20
                                                                                                                                                                                                                                                                      Query Match
Best Local :
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                                                                                                                                                                                                                                                 Matches
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SOFTWARE: PatentIn version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING NEUROLOGICAL DISORDERS AND TITLE OF INVENTION: DISEASES FILE REFERENCE: 1600.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                             Local Similarity nes 2; Conserv
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Bartel, Paul
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o. US20040226056A1
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Pred. No. 4.3e+03
0; Mismatches
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Pred. No. 4.3e+03;
0; Mismatches 4
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                                                                                                                                                                                                                                                                                           Length 20;
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Query Match
Best Local Similarity
watches 2; Conserva
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US-10-868-270-5
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; ORGANISM: Homo sapiens
US-10-776-013-616
US-10-868-270-5
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CURRENT FILING DATE: 2004-02-09
PRIOR APPLICATION NUMBER: 09/948904
PRIOR FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 09/466139
PRIOR FILING DATE: 1999-12-21
PRIOR FILING DATE: 1999-12-21
PRIOR FILING DATE: 1998-12-22
PRIOR FILING DATE: 1998-12-22
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/124120
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
                                                                                                                                                     NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 20
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                             APPLICANT: Harris, Curtis C
APPLICANT: Nagashima, Makoto
APPLICANT: Nagashima, Makoto
APPLICANT: Government of United States as represented by the Secretary of the
APPLICANT: Government of Health and Human Services
TITLE OF INVENTION: New Tumor Suppressor Gene P33ING2
FILE REFERENCE: 015280-376100US
CURRENT APPLICATION NUMBER: US/10/868,270
CURRENT FILING DATE: 2004-06-14
PRIOR APPLICATION NUMBER: US/09/513,365
PRIOR APPLICATION NUMBER: US/09/513,365
PRIOR APPLICATION NUMBER: US/09/513,365
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PRIOR APPLICATION NUMBER: US/09/513,365
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PRIOR APPLICATION NUMBER: US/09/513,365
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PRIOR FILING DATE: 2002-07-15
PRIOR APPLICATION NUMBER: 60/304775
PRIOR FILING DATE: 2001-07-13
NUMBER OF SEQ ID NOS: 695
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APPLICANT: Bartel, Paul
APPLICANT: Heichman, Karen
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING NEUROLOGICAL DISORDERS AND
TITLE OF INVENTION: DISEASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240790
PRIOR FILING DATE: 2000-10-17
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PRIOR FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: 09/975072
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                       OTHER INFORMATION:
                                                                                                                          ORGANISM: Artificial Sequence
                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 YATATL
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                          Description of Artificial Sequence: peptide 7-26 of p33ING2 (KMP1)
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33.3%;
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Pred. No. 4.3e+03;
0; Mismatches 4
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Query Match

Score 11;

DB 5;

Length 20;

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US-10-424-599-275349
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US-10-120-835-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Clone ID: PAT_MRT3847_90660C.1.pep
US-10-424-599-275349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Chou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 275349
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 12192A3 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20061.00
CURRENT APPLICATION NUMBER: US/10/120,835
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR APPLICATION NUMBER: US 60/286,630
PRIOR APPLICATION NUMBER: US 60/286,630
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: US 60/300,373
PRIOR FILING DATE: 2001-06-25
PRIOR FILING DATE: 2001-06-25
PRIOR FILING DATE: 2001-06-25
SOFTWARE: F88CSEQ for Windows Version 4.0
SEQ ID NO 67
LENGTH: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 275349, Application US/10424599 publication No. US20040031072A1 GENERAL INFORMATION:
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Matches 2; Conserv
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Publication No. US20040018189A1
GENERAL INFORMATION:
APPLICANT: Agensys, Inc.
APPLICANT: Challita-Eid, Pia
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Best Local Similarity 33.3%;
Matches 2; Conservative
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ORGANISM: Glycine max
FEATURE:
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Mitchell, Steve C.
Afar, Daniel E. H.
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Faris, Mary
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Pred. No. 5.4e
0; Mismatches
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US-10-425-115-287301
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APPLICANT: Ge, Wangmao
APPLICANT: Jakobovitz, Aya
APPLICANT: Jakobovitz, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 121P2A3 USEFUL IN TREATMENT AND
FILE REFERENCE: 51158-20061.00
CURRENT APPLICATION NUMBER: US/11/073,349
CURRENT FILING DATE: 2005-03-03
PRIOR APPLICATION NUMBER: US/10/120,835
PRIOR FILING DATE: 2002-09-12
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR APPLICATION NUMBER: US 60/286,630
PRIOR APPLICATION NUMBER: US 60/286,630
PRIOR APPLICATION NUMBER: US 60/300,373
PRIOR APPLICATION NUMBER: US 60/300,373
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PRIOR APPLICATION NUMBER: US 60/300,373
PRIOR APPLICATION NUMBER: US 60/300,373
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US-10-120-835-67
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Best Local Similarity
Watches 2; Conserve
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; ORGANISM: Homo Sapiens
US-11-073-349-67
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Publication No. US20050214211A1
GENERAL INFORMATION:
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Best Local Similarity 33.1
Matches 2; Conservative
                 Sequence 287301, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
FULE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 82
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 67
LENGTH: 28
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APPLICANT: Challita-Ei
CURRENT FILING DATE:
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Morrison, Robert K.
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Raitano, Arthur B.
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Pred. No. 5.6e+03;
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Pred. No. 5.6e+03;
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WUMBER OF SEQ ID NOS: 369326

SEQ ID NO 287301

LENGTH: 30

TYPE: PRT

CRGANISM: Zea mays

FEATURE:

ORGANISM: Zea mays

FEATURE:

ORGANISM: Zea mays

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Title: Perfect score:

Scoring table:

Sequence Sequence Sequence Sequence Sequence

Sequence

Sequence Sequence Sequence Sequence Sequence

244, Appl 45, Appl 917, App 5, Appli 5, Appli 4, Appli 6, Appli 7, Appli 11, Appl 12, Appl 12, Appl 12, Appl 13, Appl 14, Appl 14, Appl 19, Appl 19, Appl 10, Appl 10, Appl 11, Appl 11, Appl 12, Appl 13, Appl 14, Appl 15, Appl 16, Appl 17, Appl 18, Appl 19, Appl 19, Appl 19, Appl 19, Appl 19, Appl 19, Appl 19, Appl 19, Appl 19, Appl 19, Appl 19, Appl 19, Appl 19, Appl 19, Appl 19, Appl 10, Appl 11, Appl 11, Appl 12, Appl 13, Appl 14, Appl 15, Appl 16, Appl 17, Appl 18, Appl 19, Appl 10

Sequence Sequence Sequence Sequence Sequence

Sequence Sequence

Run on: OM protein -

Minimum DB Maximum DB

Database

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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seq length:
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1: /ggn2 6/ptcodata/2/pubpaa/US10 NEW PUB.pep:*

2: /cgn2 6/ptcodata/2/pubpaa/US06 NEW PUB.pep:*

3: /cgn2 6/ptcodata/2/pubpaa/US07 NEW PUB.pep:*

4: /cgn2 6/ptcodata/2/pubpaa/US08 NEW PUB.pep:*

5: /cgn2 6/ptcodata/2/pubpaa/US09 NEW PUB.pep:*

6: /cgn2 6/ptcodata/2/pubpaa/US01 NEW PUB.pep:*

7: /cgn2 6/ptcodata/2/pubpaa/US01 NEW PUB.pep:*

8: /cgn2 6/ptcodata/2/pubpaa/US01 NEW PUB.pep:*
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19
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Match Length
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         GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.
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   US-10-510-386-114
US-11-144-248-40
US-11-144-248-40
US-11-507-662-40
US-10-507-662-41
US-10-507-662-41
US-10-507-662-41
US-11-144-248-48-52
US-11-054-515-1932
US-11-054-515-1932
US-11-054-515-1932
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US-11-054-515-1936
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Sequence 114, App
Sequence 40, Appl
Sequence 40, Appl
Sequence 41, Appl
Sequence 11, App
Sequence 11, App
Sequence 15, App
Sequence 15, App
Sequence 15, App
Sequence 1932, Appl
Sequence 1932, App
Sequence 1932, App
Sequence 2054, Ap
Sequence 1915, Ap
Sequence 2164, App
Sequence 261, App
Sequence 27, App
Sequence 280, App
Sequence 280, App
Sequence 280, App
Sequence 1881, Ap
Sequence 1881, Ap
Sequence 1144, Ap
Sequence 1144, Ap
Sequence 1174, Ap
Sequence 1174, Ap
Sequence 1174, Ap
Sequence 1174, Ap
Sequence 1310, Ap
Sequence 1310, Ap
Sequence 1310, Ap
Sequence 1310, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
     Sequence 40, Application US/11144248

Publication No. US20050244408A1

GENERAL INFORMATION:
APPLICANT: Cohen, Bruce D.
APPLICANT: Beebe, Jean
APPLICANT: Miller, Penelope E.
APPLICANT: Moyer, James D.
APPLICANT: Corvalan, Jose R.
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
FILE REFERENCE: ABX-PF2
CURRENT APPLICATION NUMBER: US/11/144,248
CURRENT FILING DATE: 2002-01-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 114, Application US/10510386

Publication No. US20050244922A1

GENERAL INFORMATION:

APPLICANT: Andersen, Jens Tonne
APPLICANT: Clausen, Jens Tonne
APPLICANT: Jorgensen, Steen Troels
APPLICANT: Jorgensen, Steen Troels
APPLICANT: Rasmussen, Michael Dolberg
TITLE OF INVENTION: Improved Bacillus Host Cell
FILE REFERENCE: 10294.204-US

CURRENT APPLICATION NUMBER: US/10/510,386

CURRENT APPLICATION NUMBER: US/10/510,386

CURRENT FILING DATE: 2004-10-04

NUMBER OF SEQ ID NOS: 248

SOFTWARE: Patentin version 3.3

SEQ ID NO 114

LENGTH: 83

TYDE: DET
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US-10-510-386-114
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US-11-144-248-40
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Best Local Similarity
Matches 2; Conserv
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US-11-137-465-44
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US-10-821-234-917
US-10-927-697-697-3
US-10-997-697-7
US-10-997-697-11
US-10-997-697-11
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Pred. No. 1.1e+02;
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US-11-144-248-42
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Best Local Similarity 33...
"Arches 2; Conservative
                                                                                                                                                                                                                                                     Sequence 40, Application US/10507662 Publication No. US20050255102A1 GENERAL INFORMATION:
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LENGTH: 96
TYPE: PRT
ORGANISM: Homo mapiens
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SEQ ID NO 40
LENGTH: 96
TYPE: PRT
SEQ ID NO 40
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                                                  APPLICANT: BIOGEN, INC.
APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
TITLE OF INVENTION: ANTI-ALPHA-V BETA-6 ANTIBODIES
FILE REFERENCE: A136PCT
CURRENT APPLICATION NUMBER: US/10/507,662
CURRENT FILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: 60/364,991
PRIOR APPLICATION NUMBER: 60/364,991
PRIOR FILING DATE: 2002-03-13
PRIOR PILING DATE: 2002-03-13
PRIOR PILING DATE: 2002-11-13
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CURRENT APPLICATION NUMBER: US/11/144,248
CURRENT FILING DATE: 2005-06-02
PRIOR APPLICATION NUMBER: US/10/038,591
PRIOR APPLICATION NUMBER: 00/259,927
PRIOR APPLICATION NUMBER: 60/259,927
PRIOR APPLICATION NUMBER: 60/259,927
PRIOR FILING DATE: 2001-01-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Corvalan, Jose R.
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/259,927
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 60
                  NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn Ver. 2.1
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Pred. No. 1.2e+02;
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Pred. No. 1.2e+02;
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CURRENT APPLICATION NUMBER: US/10/507,662
CURRENT FILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: 60/364,991
PRIOR FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: 60/426,286
PRIOR APPLICATION NUMBER: 60/426,286
PRIOR FILING DATE: 2002-11-13
NUMBER OF SEQ ID NOS: 64
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 41
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-507-662-40
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                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 151, Application US/10986501 Publication No. US20050244845A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 41, Application US/10507662
Publication No. US20050255102A1
GENERAL INFORMATION:
APPLICANT: BIOGEN, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local
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                                                                                                                                                                                                                         FILE REFERENCE: PZ013P2C1
CURRENT APPLICATION NUMBER: US/10/986,501
CURRENT FILING DATE: 2004-11-12
PRIOR APPLICATION NUMBER: US/10/621,363
PRIOR FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: 09/969,730
PRIOR FILING DATE: 2001-10-06
PRIOR FILING DATE: 2001-10-06
                 PRIOR APPLICATION NUMBER: 09/244,112
PRIOR FILING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: PCT/US98/16235
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/056,371
PRIOR FILING DATE: 1997-08-19
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APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
TITLE OF INVENTION: ANTI-ALPHA-V BETA-6 ANTIBODIES
FILE REFERENCE: A136PCT
                                                                                                                                             PRIOR FILING DATE: 2000-10-06
                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/238,291
                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 09/774,639 PRIOR FILING DATE: 2001-02-01
                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: 90 Human Secreted Proteins
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TYPE: PRT
ORGANISM: Homo sapiens
APPLICATION NUMBER: 60/056,732
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Pred. No.
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1.3e+02;
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US-11-144-248-48
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 151
LENGTH: 108
TYPE: PRT
ORGANISM: Homo Bapien8
                                                           GENERAL INFORMATION:
APPLICANT: Cohen, Bruce D.
APPLICANT: Heebe, Jean
APPLICANT: Miller, Penelope E.
APPLICANT: Miller, Penelope E.
APPLICANT: Moyer, James D.
APPLICANT: Corvalan, Jose R.
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
FILE REFERENCE: ABX-PF2
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Best Local Similarity
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Best Local Similarity
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APPLICANT: Beebe, Jean
APPLICANT: Miller, Penelope E.
APPLICANT: Miller, Penelope E.
APPLICANT: Moyer, James D.
APPLICANT: Corvalan, Jose R.
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
FILE REFERENCE: ABX-PF2
CURRENT APPLICATION NUMBER: US/11/144,248
CURRENT APPLICATION NUMBER: US/10/038,591
PRIOR APPLICATION NUMBER: US/10/038,591
PRIOR FILING DATE: 2002-01-04
PRIOR FILING DATE: 2002-01-04
PRIOR FILING DATE: 2002-01-04
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PRIOR APPLICATION NUMBER: 60/056,364
PRIOR FILING DATE: 1997-08-19
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NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.1
CURRENT APPLICATION NUMBER: US/11/144,248
CURRENT FILING DATE: 2005-06-02
PRIOR APPLICATION NUMBER: US/10/038,591
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33.3%;
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Pred. No. 1.3e+02;
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Pred. No. 2.1e+02;
0; Mismatches 4
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Best Local Similarity
"---hes 2; Conserv:
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; ORGANISM: Homo sapiens
US-11-144-248-52
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US-11-054-515-1577
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CURRENT APPLICATION NUMBER: US/11/054,515

CURRENT APPLICATION NUMBER: 00/543,296

PRIOR APPLICATION NUMBER: 60/543,296

PRIOR PILING DATE: 2004-02-11

PRIOR PELICATION NUMBER: 60/580,347

PRIOR FILING DATE: 2004-06-18

PRIOR APPLICATION NUMBER: 10/293,418

PRIOR APPLICATION NUMBER: 60/331,469

PRIOR APPLICATION NUMBER: 60/331,469

PRIOR APPLICATION NUMBER: 60/331,469

PRIOR PILING DATE: 2001-11-16

PRIOR PILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR APPLICATION NUMBER: 60/380,748

PRIOR APPLICATION NUMBER: 09/880,748
US-11-054-515-1932
                       RESULT 10
                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
US-11-054-515-1577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 60/259,927
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 52
LENGTH: 236
                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILLING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILLING DATE: 2000-10-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1577
LENGTH: 241
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                                                                                                                                                                                    Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
                                                                                  182 YAASSL 187
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2; Conservat
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Pred. No. 2.1e+02;
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Pred. No. 2.2e+02;
0; Mismatches 4
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Sequence 1932, Application US/11054515 Publication No. US20050255532A1 GENERAL INFORMATION:

APPLICANT: Ruben et al.

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RESULT 11
US-11-054-515-2054
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US-11-054-515-1932
                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 10/293,418
PRIOR FILING DATE: 2002-11-14
PRIOR PELICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR APPLICATION NUMBER: 60/293,499
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PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-14
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/543,296
PRIOR FILING DATE: 2004-02-1
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2004-06-18
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CURRENT APPLICATION NUMBER: US/11/054,515
CURRENT FILING DATE: 2005-02-10
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
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CURRENT FILING DATE: 2005-02-10
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                                         DR FILING DATE: 2001-05-25

RAPPLICATION NUMBER: 60/277,379

DR FILING DATE: 2001-03-21

DR APPLICATION NUMBER: 60/276,248

DR FILING DATE: 2001-03-16

DR APPLICATION NUMBER: 60/240,816

DR FILING DATE: 2000-10-17
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Local Similarity 33.3%;
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APPLICATION NUMBER: 60/276,248
FILING DATE: 2001-03-16
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APPLICATION NUMBER: 60/293,499
FILING DATE: 2001-05-25
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APPLICATION NUMBER: 60/340,817
FILING DATE: 2001-12-19
APPLICATION NUMBER: 09/880,748
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                       Prior
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Application data removed NOS: 3247
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Pred. No. 2.2e+02;
0; Mismatches 4
                    See
                  File Wrapper or
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; SEQ ID NO 2054
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2054
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US-11-054-515-82
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PRIOR FILING DATE: 2004-06-18
PRIOR PELICATION NUMBER: 10/293,418
PRIOR PELICATION NUMBER: 60/331,469
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR APPLICATION NUMBER: 60/880,748
PRIOR APPLICATION NUMBER: 09/880,748
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            Sequence 82, Application US/11054515

Publication No. US2005025532A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind

FILE REFERENCE: FP523P3

CURRENT APPLICATION NUMBER: US/11/054,515

CURRENT FILING DATE: 2005-02-10

CURRENT FILING DATE: 2005-02-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 3247 SEQ ID NO 1915
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Best Local Similarity 33.3
Matches 2; Conservative
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Publication No. US20050255532A1
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CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR FILING DATE: 2004-02-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 24
TYPE: PRT
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PRIOR APPLICATION NUMBER: 60/543,296
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FILING DATE: 2001-05-25
APPLICATION NUMBER: 60/277,379
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Pred. No. 2.2e
0; Mismatches
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Pred. No. 2.2e+02;
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2.2e+02;
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SEQ ID NO 82
SENGTH: 244
TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-515-82
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Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 164
LENGTH: 244
TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-515-164
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Matches
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PRIOR
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523P3
CURRENT APPLICATION NUMBER: US/11/054,515
CURRENT FILING DATE: 2005-02-10
FRIOR APPLICATION NUMBER: 60/543,296
PRIOR PILING DATE: 2004-06-18
PRIOR PILING DATE: 2004-06-18
PRIOR FILING DATE: 2004-06-18
PRIOR FILING DATE: 2004-06-18
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PRIOR
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PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
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Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
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PRIOR FILING DATE: 2002-11-14
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FILING DATE: 2002-11-14
APPLICATION NUMBER: 60/331,469
FILING DATE: 2001-11-16
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APPLICATION NUMBER: 60/580,347
FILING DATE: 2004-06-18
                                                                                                                                                                                                                                                                APPLICATION NUMBER: 09/880,748
FILING DATE: 2001-06-15
APPLICATION NUMBER: 60/293,499
FILING DATE: 2001-05-25
FILING DATE: 2001-05-25
                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/340,817 FILING DATE: 2001-12-19
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FILING DATE: 2001-12-19
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Pred. No. 2.2e+02;
0; Mismatches 4
                                                                                                                               See File Wrapper or
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Search completed: November 29, 2005, 23:04:39
Job time: 3.75 secs

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US-11-054-515-261
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; ORGANISM: Homo sapiens
US-11-054-515-261
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SEQ ID NO 261
LENGTH: 244
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Best Local :
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Matches
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                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS FILE REFERENCE: PF523P3
FILE REFERENCE: PF523P3
FULRENT APPLICATION NUMBER: US/11/054,515
CURRENT ELLING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 61/293,418
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
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PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2001-03-16
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PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
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les 2; Conserv
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FILING DATE: 2001-06-15
APPLICATION NUMBER: 60/293,499
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185 YAASTL 190
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Pred. No. 2.2e+02;
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Pis Colonia Cario,